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STIC-Biotech/ChemL	ih

From:

Sent:

Walicka, Malgorzata Monday, May 23, 2005 5:45 PM STIC-Biotech/ChemLib

To:

Please search SEQ ID NO:1, 3, 4, 5, 6 in the application No. 10/622,893.

Thank you in advance.

Malgorzata A. Walicka, Ph.D. Patent Examiner Art Unit 1652, Recombinant Enzymes USPTO, Remsen Building, Room 2C76 400 Dulany St. Alexandria, VA 22313 Mail Room 2C70 Tel. (571) 272-0944, fax (571) 273-0944

STAFF USE ONLY

Searcher:_ Searcher Phone: 2-Date Searcher Picked up? Searcher Prep/Rev. Time: Online Time:_

Type of Search

NA#:/	AA#: 4
Interference:	SPDÍ:
S/L:	Oligomer:
Encode/Trans	sl:
Structure#:_	Text:
Inventor:	Litigation:

Vendors and cost where applicable

STN:_ DIALOG: QUESTEL/ORBIT:

LEXIS/NEXIS: SEQUENCE SYSTEM:

WWW/Internet:_ Other(Specify):_

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Query Match 100.0%; Score 63; DB 17; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10622893A
; Sequence 1, Application US/10622893A
; Publication No. US20050014935A1
; GENERAL INFORMATION:
    APPLICANT: Vuan, Chong-Sheng
; APPLICANT: Datta, Abhljit
; APPLICANT: Datta, Abhljit
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
; FILE REFERENCE: 46692001300
; CURRENT APPLICANTON NUMBER: US/10/622,893A
; CURRENT PILLING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 40%-100% identity to leader sequence
US-10-437-963-133890
US-10-437-963-116167
US-10-437-963-1181567
US-10-767-711-32972
US-10-767-711-32972
US-10-425-114-62751
US-10-437-963-182122
US-10-437-963-141563
US-10-437-963-141563
US-10-437-963-141563
US-10-437-963-141663
US-10-437-963-141853
US-10-437-963-141853
US-10-437-963-141872
US-10-10-160-66
US-10-437-963-11374
US-10-437-963-11374
US-10-437-963-11374
US-10-437-963-12889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-622-893A-5; Sequence 5, Application US/10622893A; Publication No. US20050014935A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGGSGDDDDLAL 12
   US-10-622-893A-1
      FEATURE:
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Sequence 5, Appli
Sequence 46722, A
Sequence 503, App
Sequence 503, App
Sequence 503, App
Sequence 40998, A
Sequence 172039,
Sequence 172039,
Sequence 172039,
Sequence 172039,
Sequence 172039,
Sequence 172039,
                                                                                                                       (without alignments)
1189.648 Million cell updates/sec
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19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                         May 27, 2005, 13:47:36 ; Search time 3.47974 Seconds
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-622-893A-1***
US-10-622-893A-5**
US-10-767-701-46955
US-10-080-170-503
US-10-080-170-503
US-10-468-356-503
US-10-477-963-200561
US-10-477-963-172039
US-10-477-963-172039
US-10-437-963-172039
US-10-437-963-17460
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                                                                                                                                                                                                                                                                        1462099 segs, 344972447 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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100.0
77.8
77.8
76.2
76.2
76.2
76.2
74.6
73.0
73.0
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Gaps

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Score

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Sequence 61, Appl Sequence 61, Appl Sequence 4812, Sequence 111374, Sequence 1120, App Sequence 120, App Sequence 129, App Sequence 129496, Sequence 129496, Sequence 107388, Sequence 107388, Sequence 107388, Sequence 107388,

Sequence 1140, Ap Sequence 1338, Ap

Sequence 1 Sequence 1

Sequence 110675,

Sequence 136, App Sequence 116, App Sequence 61, Appl Sequence 66, Appl Sequence 144342, Sequence 48120, A

Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

141563, 146049, 182133, 63251, A

Sequence Seq

Sequence Sequence Sequence Sequence Sequence

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TYPE: PRT ORGANISM: Sorghum bicolor
     SEQ ID NO 46955
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 18-21/33535) B
CURRENT APPLICATION NUMBER: 105/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46955, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Covalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUBBR: US/10/767,701
CURRENT PILLING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.8%; Score 49; DB 16; Length 102; 90.0%; Pred. No. 2.2;
                      APPLICANT: Yuan, Chong-Sheng
APPLICANT: Datta, Abhijit
APPLICANT: Datta, Abhijit
APPLICANT: Wang, Yuping
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
FILE REFERENCE: 466992001300
CURRENT APPLICATION NUMBER: US/10/622,893A
UNMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46722, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chimeric protein US-10-622-893A-5
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Matches 9; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGGSGDDDDLAL 12
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US-10-767-701-46722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-767-701-46955
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                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 472
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Sequence 503, Application US/10080170
; Publication No. US2004012132249
; Publication No. US2004012132249
; General Information:
    APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REPERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT APPLICATION NUMBER: 60/270,123
; PRIOR APPLICATION NUMBER: 60/270,123
; RIOR APPLICATION NUMBER: 60/270,123
; RIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SEQ ID NO 503
LENGTH: 64
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                                                    Length 149;
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_289.pep
US-10-767-701-46955
                                                  Score 49; DB 16;
Pred. No. 3.3;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Mycobacterium tuberculosis
US-10-080-170-503
                                                    77.8%;
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                                                  Query Match 77.8
Best Local Similarity 90.0
Matches 9; Conservative
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Matches 8; Conservative
                                                                                                                                                         91 GGSGDDDDAA 100
                                                                                                                       2 GGSGDDDDLA 11
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Best Local Similarity
Matches 8; Conserv
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Publication No. US20040123343A1
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; Sequence 40998, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; SEQ ID NOS: 63128
; SEQ ID NO 40998
; LENGTH: 230
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT PILING DATE: 2003-08-19
PRIOR FILING DATE: 2002-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 655
SOFTWARE: PATENTIN VEY: 3.2
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Pred. No. 7.4;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.2%; Score 48; DB 16; Length 64; 80.0%; Pred. No. 2; tive 1; Mismatches 1; Indels
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US-10-767-701-40998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                            ; Sequence 503, Application US/10468356; Publication No. US20040197896A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.2%;
66.7%;
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Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
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15 LGGAGDDGDLAI 26
                                             10 GGGGDDDDIA 19
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                         2 GGSGDDDDLA 11
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US-10-437-963-200561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-10-767-701-40998
                                                                                                                              RESULT 7
US-10-468-356-503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 503
LENGTH: 64
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wai
APPLICANT: Buchharuk, Brad
APPLICANT: Bucharuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERRACE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 200561
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 98-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172039
LENGTH: 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96018C.1.pep
US-10-437-963-200561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70212C.1.pep
US-10-437-963-172039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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Pred. No. 8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 172039, Application US/10437963 Publication No. US20040123343A1
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; Publication No. US20030157479A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei, Wei
APPLICANT: Would Wei
APPLICANT: Would Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.68;
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buokharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 133890
LENGTH: 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72399C.l.pep
US-10-437-963-174460
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US-10-437-963-133890
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Pred. No. 66;
0; Mismatches 1
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Pred. No. 10;
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Sequence 133890, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihna
APPLICANT: Zhou, Yihna
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-437-963-116167
; Sequence 116167, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 8; Conservative
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FEATURE:
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Best Local Similarity
      GENERAL INFORMATION:
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; Sequence 152244, Application US/10437963
; Publication No. US20040123343A1
; Canada Ca
                                                       APPLICANT: Jennings, Gary;
APPLICANT: Jennings, Gary;
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases;
FILE REPERENCE: 1700.036001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT PILING DATE: 2003-02-10
FRIOR APPLICATION NUMBER: PCT/1802/00166
FRIOR APPLICATION NUMBER: PCT/1802/00166
FRIOR FILING DATE: 2002-01-21
FRIOR FILING DATE: 2002-01-21
FRIOR FILING DATE: 2002-01-8
FRIOR FILING DATE: 2002-01-8
FRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PRECENTION VERSION 3.2
SEQ ID NO 386
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Pred. No. 6.8;
0; Mismatches 1; Indels
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US-10-437-963-152224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.0%;
90.0%;
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0°
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Matches 8; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-174460
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Vongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 116167
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69.8%; Score 44; DB 16; Length 359;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_19694C.1.pep US-10-437-963-116167
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44 VGGGGEDGDLAL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
PEATURE:
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Search completed: May 27, 2005, 14:15:01 Job time : 4.47974 secs

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3/21/2003

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 27, 2005, 13:28:05; Search time 4.55437 Seconds (without alignments) 1019.048 Million cell updates/sec

US-10-622-893A-1 Perfect score:

1 MGGSGDDDDLAL 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp290os:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* Geneseg 16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

					SUMMAKIES	
	Score		Length	DB	ΙD	Description
-	48	76.2	64	2	ABU05852	Abu05852 M. tuberc
7	46	73.0	96	7	ADX17286	Adk17286 Virus-lik
٣	43	68.3	130	Ŋ	ABJ05339	Abj05339 Human PTH
4	43	68.3	300	œ	ADQ36935	Adq36935 Cell prol
S	43	68.3	300	ω	ADQ15603	Rice
9	43	68.3	378	9	AA019572	
7	42	66.7	15	7	ADH52757	Adh52757 pBAD-TOPO
60	42	66.7	17	Ŋ	ABG68924	
6	42	66.7	17	ß	ABG68919	Abg68919 Lawsonia
10	42	66.7	157	8	ADI45189	Adi45189 Rice isop
11	42	66.7	402	4	ABG12558	Abg12558 Novel hum
12	42	66.7	404	9	ABU35241	Abu35241 Protein e
13	42	66.7	409	8	ADL05698	_
14	42	66.7	447	œ	AD142677	Adi42677 Plant tra
15	42	66.7	447	8	AD002925	Ado02925 Thalecres
16	42	66.7	581	4	ABB59833	Abb59833 Drosophil
17	42	66.7	730	4	ABB61435	Abb61435 Drosophil
18	42	66.7	784	4	ABB62115	Abb62115 Drosophil
19	42	66.7	858	œ	ADS20230	Ads20230 Human agg
20	42	66.7	1138	7	AB077206	Abo77206 Pseudomon
21	42	66.7	1926	4	AAG84915	Aag84915 Shrimp wh
22	41.5	62.9	21	S	AAU75830	-
23	41	65.1	32	2	ABG80719	Abg80719 Human IgG
24	41	65.1	32	œ	ADI40815	
25	41	65.1	47	ഗ	ABG80720	Abq80720 Human IqG

Adi40817 pCep-SP-E Aau22386 Human car Add6754 Human car Ad50772 Human car Aab53618 Human cal Ab594342 Human res Ab696454 Human res Ab696654 Human res Ab696654 Human res Ab696654 Human res Ab696654 Human res Ab696651 Mouse res Ab696651 Mouse res Ad340821 Mouse Res Ad40821 Resistin Ad568201 Human pro Ad568201 Human pro Ad568201 Human hea Ab694339 Mouse mpr	Addzily mrrr-er- Adj70832 Human hea
ADI 40817 AAV122386 AAV122386 ADI 407772 ADI 5125 ABG80654 ABG80654 ABG80654 ABG80653 ABG80652 ADI 40821 ADI 6821 ADI 6821	ADJ70832
247888774440089008 847888888888888888888888888888888888	
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ALIGNMENTS

Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy. M. tuberculosis and M. leprae marker protein #503. ABU05852 standard; protein; 64 AA. 22-FEB-2001; 2001US-0270123P. 22-FEB-2002; 2002WO-IB001973. Mycobacterium tuberculosis. Mycobacterium leprae. 08-APR-2003 (first entry) (INSP) INST PASTEUR WPI; 2002-759885/82. WO200274903-A2. 26-SEP-2002. ABU05852; Cole S; ABU05852

Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.

Claim 17; Page 714-715; 874pp; English.

This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from

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Gaps

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Indels

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RESULT 2 ADK17286

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Target peptide production; fusion peptide; protease-susceptible linker; parathyroid hormone; PTH; high expression rate;
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                        Human PTH(1-34)-ZAQ ligand fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 87-88; 103pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.3%; Score 43;
80.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ36935 standard; protein; 300 AA.
                                                                                                                                                                                                     ABJ05339 standard; protein; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001; 2001WO-JP009476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-2000; 2000JP-00331170.
27-JUN-2001; 2001JP-00195522.
90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical application.
                                                                                                                                                                                                                                                                                  (first entry)
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Matches 8; Conservative
                      9; Conservative
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                                                            12
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                                                                                                 10 GSGDDDDKAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada T, Suenaga M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-417275/44.
N-PSDB; ABT06827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GSGDDDDKAV
                                                            3 GSGDDDDLAL
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200236762-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                  08-NOV-2002
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                                                                                                                                                                                                                                             ABJ05339;
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                      Matches
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ADQ36935
                                                                                                                                                                RESULT 3
                                                                                                                                                                                    ABJ05339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and at least one antigen, which is a protein or peptide of interleukin (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a core particle with at least one first attachment site and at least one antigen with at least one second attachment site, where the antigen is a protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site antigen or antigenic determinant. The second attachment site antigen or antigenic determinant. The second attachment site is capable of association to the first attachment site, and where the antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The compositions are useful as medicaments, or for manufacturing a medicament or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or Hodgkin's lymphoma and related diseases. This sequence is used to
Mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising an ordered and repetitive antigen or antigenic determinant array, useful as a medicament, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition comprising a virus-like particle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiallergic, antiasthmatic, cytostatic, vaccine, virus-like particle, interleukin, IL-5, IL-13, eotaxin, repetitive antigen array, allergic eosinophilic disease, asthma, Hodgkin's lymphoma.
                                                                                                                                           Gaps
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                                                                                                     Length 64;
                                                                                                                                           1; Indels
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                                                                                                 Score 48; DB 5;
Pred. No. 3.6;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             generate the compound of the invention
                                                                                                                                                                                                                                                                                                                        ADK17286 standard; peptide; 96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CYTO-) CYTOS BIOTECHNOLOGY AG
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18-JAN-2002; 2002US-00050902.
21-JAN-2002; 2002WO-IB00166.
19-JUL-2002; 2002US-0396636P.
                                                                                                   76.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                           8; Conservative
                      method of the invention
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                                                                                                   Query Match
Best Local Similarity
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                                                            Sequence 64 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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Production of target peptide comprises cleavage of fusion peptide with parathyroid hormone peptide for efficient manufacture of target peptide without the need to remove N-terminal methionine.
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1; Mismatches
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73.0%; Score 46; DB 7; Length 96;

Query Match

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26-DEC-2002; 2002US-0436564P
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                                       Cooper
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                                                                                                                                                                                                                                                                                The present invention relates to an isolated nucleic acid molecule encoding a cell proliferation-related polypeptide. The nucleic acid molecule and the encoded polypeptide, and methods are useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops. The present sequence represents a cell proliferation-related polypeptide. The present sequence is published separately from the main body of the specification as EPO data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rice; stress-related protein; plant maturation; plant development; plant proliferation, plant senescence; plant disease-resistance; plant stress response; transgenic plant; pest tolerance; herbicide tolerance; biotic stress tolerance; amproved nutritional value; increased yield; increased proliferation.
                           cell proliferation related polypeptide; cell proliferation; senescence; differentiation; stress response.
                                                                                                                                                                                                              New nucleic acid molecule encoding a cell proliferation-related polypeptide, useful for modulating cell proliferation, senescence, differentiation, development, and stress response in plants, and for producing enhanced food crops.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           68.3%; Score 43; DB 8; Length 300; 66.7%; Pred. No. 1.1e+02;
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          Cell proliferation-related polypeptide #45
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                                                                                                                                                                                                                                                               Claim 28; SEQ ID NO 94; 408pp; English.
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                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                23-DEC-2003; 2003WO-US041200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-2003; 2003WO-US041098.
                                                                                                                                    26-DEC-2002; 2002US-0436565P
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                          Sequence 300 AA;
                                                                           WO2004061122-A2
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                                                        Oryza sativa
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                                                                                              22-JUL-2004
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                                                                                                                                                                         Cooper B;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequences of rice stress-related proteins. The DNA and protein sequences of the invention are useful for regulating and controlling plant maturation and development, including proliferation, senescence, disease-resistance, or stress response. They are also useful for producing transgenic plants having improved properties, e.g. tolerance to pests, herbicides, or biotic or abiotic stresses, improved nutritional value, increased yield or proliferation, or improved structure causing less loss from lodging or shattering. The present amino acid sequence represents a rice stress-related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substance PF1022; biosynthesis; transgenic; chorismic acid; anthelmintic; phenylalanine; p-aminophenylpyruvic acid; pharmaceutical;
                                                                                                                                                                                                                New isolated nucleic acids and proteins, useful for producing transgenic plants having improved properties, e.g. tolerance to peets, herbicides, or biotic or abiotic stresses, improved nutritional value, or increased yield or proliferation.
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66.7%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                       Claim 28; SEQ ID NO 12; 551pp; English
(SYGN ) SYNGENTA PARTICIPATIONS AG.
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Best Local Similarity
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having a 16S rRNA DNA sequence fully defined in the specification, provided that the bacteria is not a strain of Porphyromonas gingivalis designated as dog 20B. The invention has antiinflammatory applications whilst the bacteria and polymucleotide may be useful for preparing a whilst the bacteria so preventing periodontal disease in companion animals. The current sequence is that of the Porphyromonas-related vector amino-terminal peptide of the invention.
                       The present invention relates to transformants capable of producing PF1022 substance derivatives. These were obtained by transferring a gene participating in the biosynthesis pathway from choriamic acid to paminophenylpyruvic acid (biosynthesis gene) into a phenylalanine-requiring host derived from an organism producing the PF1022 substance. The transformants are producing PF1022 substance derivatives by fermentation, for use as pharmaceuticals or veterinary drugs. The present sequence is a fragment of a Myroclia sterilia protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pigmented anaerobic bacteria, useful for preparing a vaccine or preventing periodontal disease in companion animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated pigmented anaerobic bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pigmented anaerobic bacterium; 16S rRNA; antiinflammatory; vaccine; periodontal disease; OprF; pBAD-TOPO:OprF vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 6; Length 378;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardham JM, King KW, Krishnan R, Mcgavin DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBAD-TOPO:OprF vector amino-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; SEQ ID NO 136; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH52757 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2002; 2002WO-IB005539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-2001; 2001US-034299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.C
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GEGDDDDALL 247
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003054755-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ADHIESTST 7
ADHIESTST 8
ADHIES
X88888888888X8
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The inferior of a lawsonia spo. polypeptides with a B-cell or T-cell epitope of a Lawsonia spo. polypeptide such as filbs, filk, ntrC, gluh, moth, moth, tlyC, ytfM or ytfM polypeptides. (I) is useful for dentifying whether or not a portione or avian animal has suffered from a past infection, or is currently infected, with Lawsonia spo or a microorganism that is immunologically cross-reactive with Lawsonia spo. Antibodies are useful for diagnosing infection of a portion or avian animal by Lawsonia spp. or a microorganism that is immunologically cross-reactive with Lawsonia spp.

Antibodies are useful for diagnosing infection of a portion or avian animal by Lawsonia spp. A mucleit acid encoding a Lawsonia spp. Immunogen is useful as probes or primers for detecting Lawsonia spp. Immunogen is useful as probes or primers for detecting Lawsonia spp. Immunogen is useful as probes or primers for detecting Lawsonia spp. Immunogen is useful as probes or primers for detecting Lawsonia spp. Immunogenia min a biological sample derived from a porcine or immals against intestinal diseases collectively known as intestinal denominations of the proplylaxis and treatment of proliferative enterities and centerities. (I) is also useful in vaccines for the prophylaxis and treatment of protein related peptide represents a lawsonia intracellularis immunogenic protein related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polypeptide comprising epitope of Lawsonia spp. polypeptide such as fihB, fl1R, ntrC, glnH, motA, polypeptides, useful in vaccines for treatment of porcine proliferative enteropathy in pigs and
                                                                                                                                                                                                    ytfM; ytfN; porcine;
                                                                                                                                                                                                Immunogen, fihB; fliR; ntrC; glnH; motA; motB; tlyC; ytfM; ytfN; porcir pig; avian; bird; porcine proliferative enteropathy; PPB; intestinal adenomatosis complex; porcine intestinal adenomatosis; PIA; necrotic enteritis; proliferative haemorrhagic enteropathy; regional ileitis; haemorrhagic bowel syndrome; vaccine; antibacterial; porcine proliferative enetritis; Campylobacter spp.-induced enteritis.
                                                                                                                                                        Lawsonia intracellularis immunogenic protein related peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated or recombinant immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strugnell RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGRI-) AGRIC VICTORIA SERVICES PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 153; 155pp; English.
                    ABG68924 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Good RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-2001; 2001WO-AU001462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0-NOV-2000; 2000AU-00001381
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                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       WO200238594-A1.
                                                                                                          10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                ABG68924;
ABG68924
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                                                                                                                                                                                                                                            Gaps
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Dreier KJ

3

Gaps

.. 7

ch 66.7%; Score 42; DB 5; Length 17; 1 Similarity 85.7%; Pred. No. 7.9; 12; Conservative 0; Mismatches 0; Indels

Best Local Similarity

Query Match Matches

7

Gaps

2;

Score 42; DB 7; Length 15; Pred. No. 6.9; 0; Mismatches 0; Indels

66.7**%**; 85.7**%**;

Best Local Similarity 85.7 Matches 12, Conservative

Query Match

1 MG-GSGDDDD-LAL 12

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ñ

Gaps

5

Length 17; Indels

5,

Score 42; DB : Pred. No. 7.9; 0; Mismatches

(first entry)

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dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase;
gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone;
phylloquinone; mevalonate pathway; phytosterol; brassinosteroid;
ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghassemian M, Briggs SP, Cooper B, Glazebrook J;
katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;
                                                                                                                                                                                                                                                                                                                                                                          isoprenoid blosynthesis; plant; isopentenyl diphosphate; IPP;
                                                                                                                                                                                                                                                                                                                                     Rice isoprenoid biosynthesis-associated protein #60.
                                                                                                                                                                                                                   ADI45189 standard; protein; 157 AA
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04-APR-2002; 2002US-0370620P
04-APR-2002; 2002US-0370743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002; 2002US-00259194
Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                               1 MG-GSGDDDD-LAL 12
                                                                                                                 MGSGSGDDDDKLAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANGE B M.
GHASSEMIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLAZEBROOK J. GOFF S A.
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COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KATAGIRI F.
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MOUGHAMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
                                                                                                                                                                                                                                                                                              22-APR-2004
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                                                                                                                                                                                                                                                          ADI45189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOUG/)
(PROV/)
(RICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KATA/)
(KREP/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAZ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu T;
                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                   ADI45189
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                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated or recombinant immunogenic polypeptide (I) which comprises, minds or cross-reacts with a B-cell or T-cell epitope of a Lawsonia spp. polypeptides. (I) is useful filk, ntrC, gluH, motA, motB, tlyC, ytfM or ytfW polypeptides. (I) is useful for identifying whether or not a porcine or avian animal has suffered from a pertial infection, or is currently infected, with Lawsonia spp. or a microorganism that is immunologically cross-reactive with Lawsonia spp. Or animal by Lawsonia spp. or a microorganism that is immunologically cross-reactive with Lawsonia spp. or a microorganism that is immunologically cross-reactive with Lawsonia spp. or creative with Lawsonia spp. . A nucleic acid encoding a Lawsonia spp. creative with Lawsonia spp. . A nucleic acid encoding a Lawsonia spp. creative with Lawsonia spp. or animal subject. (I) is preferably useful for vaccinating porcine or avian animal subject. (I) is preferably useful for vaccinating porcine or animals against intestinal diseases collectively known as porcine
                                                                                                                                                                                                                                                                                                             Immunogen; fihB; fliR; ntrC; glnH; motA; motB; tlyC; ytfM; ytfN; porcine; pig; avian; bird; porcine proliferative enteropathy; PPE; intestinal adenomatosis complex; porcine intestinal adenomatosis; PIA; necrotic entertis; proliferative hemenorthagic enteropathy; regional lieitis; haemorrhagic bowel syndrome; vaccine; antibacterial; porcine proliferative enetritis; Campylobacter spp.-induced enteritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide comprising epitope of Lawsonia spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, polypeptides, useful i vaccines for treatment of porcine proliferative enteropathy in pigs and
                                                                                                                                                                                                                                                                          Lawsonia intracellularis immunogenic protein related peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strugnell RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 152; 155pp; English
                                                                                                                                                        ABG68919 standard; peptide; 17 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-2000; 2000AU-00001381
17-NOV-2000; 2000US-0249596P
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                      12
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                                                                                                                                                                                                                                   (first entry)
                      MG-GSGDDDD-LAL
                                            1 MGSGSGDDDDKLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-557448/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                    ABG68919
                                                                                                                   RESULT
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The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polynucleotide, a host cell comprising the expression cassette, and a transgenic plant comprising the expression cassette. The polypeptides and polynucleotides include those associated
                                                                                                                                                                  New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 120; 117pp; English.
WPI; 2004-090562/09.
N-PSDB; ADI45188.
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proliferative enteropathy (PPE), previously known as intestinal adenomatosis complex, porcine intestinal adenomatosis (PIA), necrotic enteritis, proliferative haemorrhagic enteropathy, regional lieitis, haemorrhagic bowel syndrome, porcine proliferative enetritis and campylobacter spp.-induced enteritis. (I) is also useful in vaccines for the prophylaxis and treatment of PPE in birds. This sequence represents a Lawsonia intracellularis immunogenic protein related peptide

Sequence 17 AA;

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with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid cancelly the biosynthesis of gibberellins, the biosynthesis of carotemoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, biosynthesis of monterpenes and sesquiterpenes, protein prenylation, and biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polynucleotides. The polynucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a coloss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from USPPTO at the colon of the connection of the produce of the colon of the produce and form the form of the plants as well as mater of the printed specification, but was obtained in electronic form the directly from USPPTO at the plants of the printed specification, but was obtained in electronic form the part of the printed specification, but was obtained in electronic form at the plants and the correspondence and the corres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       segdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence represents a Rice isoprenoid biosynthesis-associated protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 8; Length 157;
Pred. No. 79;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #12549.
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2000US-00649167
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Best Local Similarity 8/...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 157 AA;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

Claim 20; SEQ ID NO 42917; 103pp; English.

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymorleotides are also used an diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) to to traat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymorleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Esquences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                Length 402;
                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 4; Lengtn rv...
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #20768.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU35241 standard; protein; 404 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-077-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.50,
T; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 402 AA;
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Wall D,
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued to polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for the tay against a biological pathway in which a proliferation or that inhibits cellular proliferation of an influence or cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture compound that inhibits proliferation of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains in speament in a culture or collection of the strains or screening for homologous nucleic acids are useful for confileration of an organism. The antisense incleic acids are useful for required for proliferation to isolate candidate molecules for rational cultured for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this patent did not forma part of the printed specification, but was obtained to in electronic format directly from MIPO at
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87.5%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis; infection.
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Matches 7; Conservative
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                                                  encoding an Moraxella
                                                                                                                                                                                                                                                                                                                                                                                         transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flowering; flowering; flowering; flowering; flowering partern; apical dominance; trichome; stem morphology; root growth; root hair; sed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; gene; ds.
                                              The invention relates to an isolated nucleic acid encoding an Moraxells catarrhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents the amino acid sequence of a M. catarrhalis protein.
                                                                                                                                                                              Gaps
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Keddie J,
                                                                                                                                                    Length 409;
                                                                                                                                                  Score 42; DB 8; Length 405
Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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Ratcliffe O, Adam LJ, Reuber TL,
Dubell AN, Pineda O, Yu G;
                         Disclosure; SEQ ID NO 3384; 429pp; English.
                                                                                                                                                                                                                                                                                                ADI42677 standard; protein; 447 AA.
caused by Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                         Plant transcription factor #408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2003; 2003US-00374780
                                                                                                                                                  Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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RIECHMANN J L.
                                                                                                                                                                                                                               386 GGDGDDDD 393
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REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
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PINEDA O.
YU G.
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HEARD J E.
HAAKE V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-132245/13
                                                                                                                                                                                                       2 GGSGDDDD
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                                                                                                                            Sequence 409 AA;
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                                                                                                                                                                                                                                                                                                                                                22-APR-2004
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(HEAR/)
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                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                   ADI42677
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2000WO-US009448. 2000US-00713994. 2001US-00819142. 2001US-00837444. 2002US-00958131.

16-NOV-2000;

2002US-00225066. 2002US-00225067. 2002US-00171468

27-MAR-2001; 2 17-APR-2001; 2 30-JAN-2002; 2 14-JUN-2002; 2 09-AUG-2002; 09-AUG-2002;

2002US-00225068

17-DEC-2002; 2002US-0434166P 25-FEB-2003; 2003US-00374780

ZHANG J. FROMM M E. HEARD J E. RIECHMANN J L.

ZHAN/) HEAR/) ADAM L J. BROUN P E. PINEDA O. REUBER T L. KEDDIE J S.

(PINE/) (REUB/)

(ADAM/) (BROU/)

RIEC/

JIANG C.

JIAN/

χa G.

YUGG/

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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the complement. The method of the complement of the complement. The method of the chancing of the sensitivity; disease resistance; sugar sensing; early or late flowering; sensitivity; disease resistance; sugar sensing; early or late flowering; pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichomes development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed blochemistry; increase in root anthocyanins; increase in plant cares anthocyanins; or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in blochometric search methods This is the amino acid sequence of a plant transcription factors isolated in the invention, that can be used in the transcription of a transgenic plant with altered traits.
New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                          Claim 1; SEQ ID NO 1140; 435pp; English.
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Sequence 447 AA;

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66.7%; Score 42; DB 8; Length 447
72.7%; Pred. No. 2.4e+02;
cive 0; Mismatches 3; Indels
Query Match
Best Local Similarity 72.7,,
Best Local Similarity 72.7,,
                                                                                2 GGSGDDDDLAL 12
                                                                                                             75 GGGÖDDALGL 85
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RESULT 15

ADO02925 standard; protein; 447 AA. AD002925;

01-JUL-2004 (first entry)

Thalecress transcription factor, Rice orthologue #66.

cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; agar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature sensecence; delayed sensescence; lethality; necrosis; plant size; leaf morphology; secondary metabolism; light response; shade avoidance. Rice; transcription factor; plant; transgenic; abiotic stress;

Oryza sativa.

US2004045049-A1.

04-MAR-2004.

10-APR-2003; 2003US-00412699

13-SEP-1999; 99US-00394519.
21-JAN-2000; 2000US-00489376.
17-FEB-2000; 2000US-0056720.
22-MAR-2000; 2000US-005333029.
22-MAR-2000; 2000US-005333029.

CREELMAN R A. DUBELL A N. RATCLIFFE O. SAMAHA R S. PILGRIM M L. SHERMAN B K Fromm ME, KUMIMOTO R. Zhang J, (SAMA/) (PILG/) (CREE/) (RATC/) SHER/) DUBE/) ö Gaps ö Length 447;

Broun PE; Yromm ME, Heard JE, Riechmann JL, Adam LJ, Broun Pl Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS; Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R; Pineda O, Re Pilgrim ML, Sherman BK;

WPI; 2004-225755/21.

New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

Claim 1; SEQ ID NO 1339; 213pp; English.

The invention relates to a transgenic plant comprises a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a gequence or its complementary consequence comprising a gequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as AD00158 - AD0013519 - AD0013559. Also included are using a transgenic constitutive, inducible or tissue-specific promoter and a recombinant polymucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polymucleotide sequence that is subject to a regulatory effect of any of the polymeleotide sequence that is subject to a regulatory effect of any of transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered contining, germination in cold conditions, freezing tolerance to explain to the early colerance to thilling, germination in cold conditions, freezing tolerance to console to hormone sensitivity, reduced sensitivity to nitrogen limitation, altered susceptibility to response to ethylene, disease resistance, altered susceptibility to Evrysiphe, altered susceptibility to Pusarium, altered susceptibility to Erysiphe, altered susceptibility to Pusarium, altered susceptibility to Erysiphe, altered susceptibility to Pusarium, altered susceptibility or Erysiphe, altered susceptibility to Pusarium, altered susceptibility to Sclerotina, altered susceptibility to germination and seedling vigor, early flowering, laterial change; a change in the prido of flowering, a lack of a shoot meristem, reduced meristeme cell

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differentiation, ancered purifications, and anatoming partern, reduced aptical dominance, reduced trichome development, altered stem morphology, increased root growth, increased root hairs, altered stem morphology, increased root growth, increased root hairs, altered seed development, altered cell crowled plant size, a change in leaf morphology, increased leaf size, a change in leaf morphology, increased leaf size, a change in leaf morphology, increased altered leaf development, increased leaf size, altered seed shape, change in leaf blochemistry, increased leaf size, altered seed shape, change in leaf blochemistry, increased leaf anthoryanins, an alteration in leaf prenyl lipid content, increased leaf anthoryanins, an alteration of leaf fatty acid content, an alteration of leaf glucosinolate content, change in seed fatty acid content, increase in seed fatty acid content, decrease in seed fatty acid content, decrease in seed fatty acid content, increase in seed fatty acid content, decrease in seed fatty acid content, increase in seed protein content, decrease in seed fatty acid content, increase in seed protein content, decrease in seed fatty acid content, increase in seed protein content, increase in secd content, increase in plant anthocyanins, and alteration in clight response or shade avoidance. The present sequence represents an element of content content sequence represents an element of content content sequence represents an element of content content content sequence represents and alteration in clight response or shade avoidance. The present sequence represents an element sequence of a thalecress transcription factor isolated from Rice.
differentiation, altered phyllotaxy, altered branching pattern,
$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 447 AA;

ö Gaps ö 66.7%; Score 42; DB 8; Length 447; 72.7%; Pred. No. 2.4e+02; ive 0; Mismatches 3; Indels Query Match
Best Local Similarity 72.7
Matches 8; Conservative

2 GGSGDDDDLAL 12 75 Š 셤

Search completed: May 27, 2005, 13:43:51 Job time: 7.55437 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

on: Run

May 27, 2005, 13:34:21; Search time 0.921109 Seconds (without alignments) 1253.491 Million cell updates/sec

US-10-622-893A-1 63

1 MGGSGDDDDLAL 12 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 79:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	_	_	_	folded gastrulatio	probable membrane	C29E4.2 protein -	hypothetical prote		hypothetical prote	probable ATP-bindi	protein disulfide-	protein disulfide-	CDC48-like protein	phosphatidylinosit	DNA-directed RNA p	daunorubicin C-13	prostatic spermine	probable secreted	hypothetical prote	hypothetical prote	cellulase (EC 3.2.	Ca2+-transporting	protein B0464.2 [i	hypothetical prote	polyketide synthas	Band 3 anion trans	hypothetical prote	hypothetical prote
SUMMARIES	ΩI	B70512	H84708	T27007	S46825	A53064	T02823	S44769	S54493	T18403	B87376	T36100	ISHUSS	ISBOSS	T46169	S66672	RNBY3C	C82643	A29561	E95914	G84251	G95405	JS0174	T52654	D88556	S28279	T30283	S03991	T30047	H70753
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	Query Match Length	64	240	894	582	730	818	918	943	1360	84	489	508	510	815	875	251	294	334	353	504	539	825	1074	1150	1274	6420	58	185	Ø.
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	Score	48	44	43	42	42	42	42	42	42	41	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39	39	39
	Result No.	-	7	e	4	Ŋ	9	7	8	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

TOM (target of myb	protein disulfide-	hypothetical prote	flagellar M-ring p	ATP sulfurylase GT	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	homeotic protein l	hypothetical prote	probable serine/th	protein disulfide-	lysine-tRNA ligase	hypothetical prote
T51543	ISMSSS	869069	F83508	D83091	T14612	T19879	C87074	S09814	D83161	B40722	B84376	C70986	ISRTSS	A71246	T23700
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407	509	579	598	633	633	810	63	157	218	288	360	476	508	523	539
61.9	61.9	61.9	61.9	61.9	61.9	61.9	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3
		6	6	39	39	39	38	38	38	38	38	38	38	38	38
39	39	m	٠.,												

ALIGNMENTS

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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
hypothetical protein Rv2111c - Mycobacterium tuberculosis (strain H37RV)
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CiAccession: Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-64 < COL>

A;Cross-references: UNIPROT:033246; GB:297559; GB:AL123456; NID:g3261820; PIDN:CAB10702. A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv2111c

Gaps ö Length 64; 1; Indels DB 2; Score 48; DB 2; Pred. No. 0.42; 1; Mismatches 76.2%; 80.0%; Query Match
Best Local Similarity 80.0
Matches 8; Conservative

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g Š

"Mypothetical protein At2g30480 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Reb-2001 #sequence_revision 02-Reb-2001 #text_change 09-Jul-2004 (Spacession: H84708 (Spacession: H84870; Multiples) (Spacession: H84870; Multiples) (Spacession: H84870; Multiples) (Spacession: H84870; Multiples) (Multiples) (Multipl

A; Accession: H84708

A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-240 <STO>

A; Cross-references: UNIPROT:023686; GB:AE002093; NID:g2257712; PIDN:AAB63096.1; GSPDB:GN

C;Genetics:

A;Gene: At2g30480 A;Map position: 2

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Cispecies: Leishmania major
Cidate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Cidate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Cidates: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Rimyler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; F
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Reference number: A81455; MUID:99178987; FMID:10077609
A;Accession: C81459
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-818 <PYL>
A,CTOSE-references: UNIPROT:Q25353; GB:AE001274; NID:G3264850; PIDN:AAC24646.1; PID:G3264
A,Experimental source: strain MHOM/IL/81/Friedlin
A;Status: preliminary
A;Molecule type: mRNA
A;Redidues: 1-730 cCOS>
A;Cross-references: UNIPROT:P40795; GB:U03717; NID:g430722; PIDN:AAA18955.1; PID:g430723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein L1231.1 [imported] - Leishmania major (strain Friedlin)
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C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44769
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C;Superfamily: Leishmania major probable membrane protein L1231.1
C;Keywords: transmembrane protein
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50;
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R;Wilson, R.
submitted to the EMBL Data Library, September 1993

A;Description: Sequence of the C. elegans cosmid C29E4.

A;Refarence number: S44738

A;Accession: S44769

A;Actus: preliminary

A;Molecule type: DNA

A;Residues: 1-918 <WIL>
A;Cross-references: EMBL:L23651; NID:g388575; PID:g388580
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                             Score 42; DB Pred. No. 50; 1; Mismatches
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                                                                                                                                                                                                                                                                              A; Cross-references: FlyBase: FBgn0000719
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illarity 87.5%;
Conservative
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Best Local Similarity 77.8%;
Matches 7; Conservative
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513 IGGRGDDDD 521
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Best Local Similarity
Matches 7; Conserv
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                                                                                                       A; Accession: A53064
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A;Cross-references: UNIPROT:Q9U297; EMBL:AL110490; NID:e1542263; PIDN:CAB54451.1; CESP:Y
A;Experimental source: clone Y48B6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S46825
A;Molecule type: DNA
A;Readiues: 1-585 <FAV>
A;Cross-references: UNIPROT:P38748; EMBL:U11582; NID:g2289793; PID:g508747; GSPDB:GN0000
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C,Superfamly: fission yeast probable zinc finger protein SPAC16E8.13; RING finger homol
F;236-285/Domain: RING finger homology <RNG>
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folded gastrulation (fog) precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53064
                                                                                                                                                                                                                                                                            hypothetical protein Y48B6A.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Saccharomyces cerevisiae
Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
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     69.8%; Score 44; DB 2; Length 240; 77.8%; Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.3%; Score 43; DB 2; Best Local Similarity 77.8%; Pred. No. 43; Matches 7; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                           R;Wall, M.
ubmitted to the EMBL Data Library, September 1999
A;Reference number: Z20297
A;Accession: T27007
                                                   2; Mismatches
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A,Introns: 71/2; 146/2; 510/1; 558/2
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Cross-references: SGD:S0001002
                         Best Local Similarity 77.8
Matches 7; Conservative
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163 VGGTGDDDD 171
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     Query Match
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C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: B87376
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-84 <STO>
A;Cross-references: UNIPROT:Q9A9G6; GB:AE005673; NID:g13422314; PIDN:AAK23006.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T36100
R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21596
A;Accession: T36100
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1489 <SAU>
A;Cross-references: UNIPROT:Q9X873; EMBL:AL049661; PIDN:CAB41216.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
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C;Species: Homo sapiens (man)
C;Accession: Aliou-1992 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: Alious Ballala, A30055; A29787; A26632; A42791; I33178; F61002
R;Tasanen, K.; Parkkonen, T.; Chow L.T.; Kivirikko, K.I.; Pihlajaniemi, T.
A;Title: Chem. 263, 16218-16224, 1988
A;Title: Characterization of the human gene for a polypeptide that acts both as the beta A;Reference number: A31913; MUID:89034087; PMID:2846539
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A;Residues: 1-508 <TA2>
A;Cross-references: GB:J04049; GB:J04050; GB:M22803; GB:M22804; GB:M22805; GB:M22806; NI
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ATP-binding protein - Streptomyces coelicolor
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48;
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Pred. No.
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Pred. No.
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A;Residues: 1-118;209-508 <TAS>
A;Cross-references: UNIPROT:P07237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%;
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ilarity 66.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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GGHGEDDELA 44
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
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T36100
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A; Residues: 1-943 <LYE>
A; Residues: 1-943 <LYE>
A; Cross-references: UNIPROT: P39523; EMBL: Z49273; NID: 9809577; PIDN: CAA89273.1; PID: 98095
R; Pandit, S.; Sternglanz, R.
submitted to the EMBL Data Library, December 1992
A; Reference number: S48514
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C;Species: Plasmodium falciparum
C;Species: Dlasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18403
R;Accession: T18403
R;BARALE, J.C.; ATTALBONNEFOY, G.; BRAHIMI, K.; DASILVA, L.P.; LANGSLEY, G.
Mol. Biochem. Parasitol. 87, 169-181, 1997
A;Title: Plasmodium-falciparum asparagine and aspartate rich protein-2 is an evolutionar A;Reference number: Z08834; MUID:97391121; PMID:9247928
A;Accession: T18403
A;Accession: T18403
A;Accession: T18403
A;Molecule type: MRNA
A;Molecule type: MRNA
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A;Cross-references: UNIPROT:Q94649; EMBL:Y08924; NID:e1008106; PID:e1154303; PIDN:CAA701
C;Genetics:
A;Gene: aarp2
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                                                                                                                                                                                                                                                                                                                  N.Alternate names. hypothetical protein YM8564.06
C.Species: Saccharomyce cerevisiae)
C.Species: Saccharomyce cerevisiae
C.Species: C.Species:
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A,Residues: 770-943 <PAN>
A,Cross-references: EMBL:L07650; NID:g349191; PIDN:AAA35122.1; PID:g349192
C,Genetics:
A,Cross-references: SGD:S0004731
                                           Gaps
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87.5%; Pred. No. 97;
ive 0; Mismatches 1; Indels
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B87376
hypothetical protein CC1022 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
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Pred. No. 66;
0; Mismatches 1; Indels
                                           Indels
                                           1,
       d. No. 64;
Mismatches
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       Pred. No.
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   87.5%;
   Best Local Similarity 87.8
Matches 7; Conservative
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Matches 7; Conservative
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Best Local Similarity '
                                                                                                                                                                               512 ĠĠĠĠĎĎĎ 519
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                                                                                                             GGSGDDDD 9
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procenn disulfide-isomerase (BC 5.3.4.1) precursor - bovine NyAlternate names: cellular thyroid hormone-binding protein; endoplasmic reticulum protein NyContains: procollagen-proline dioxygenase (BC 1.14.11.2) beta chain; thyroxine deioding C;Species: Bos primigenius taurus (cattle) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yamauchi, K.; Yamamoto, T.; Hayashi, H.; Koya, S.; Takikawa, H.; Toyoshima, K.; Horiuch Biochem. Biophys. Res. Commun. 146, 1485-1492, 1987.
A;Title: Sequence of membrane-associated thyroid hormone binding protein from bovine live A;Reference number: A26829; MUID:87298601; PMID:3619939
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A,Note: the authors translated the codon TTC for residue 175 as Leu
C;Comment: This enzyme catalyzes the rearrangement of both intrachain and interchain discipled in the codon of the codon 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C'Accession: T46169
R;NyAkatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; P. submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23025
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A;Introns: 10/2; 65/3; 142/1; 397/3; 589/3
A;Note: T4D2.160
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind:
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A,Experimental source: cultivar Columbia; BAC clone T4D2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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87.5%; Pred. No. 50;
:ive 1; Mismatches
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F,312-343/Disulfide bonds: #status predicted
                                                                                                       Score 41;
Pred. No.
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                                                                                                       65.1%;
87.5%;
                                                   Query Match
Best Local Similarity 87.5
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Best Local Similarity 87.5
Matches 7; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-815 <NYA>
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: liver K; Robinson, E.A.; Appella, E.; Merlino, G.T.; Pastan, J. Biol. Chem. 262, 11221-11227, 1987
A; Title: The nucleotide sequence of a human cellular thyroid hormone binding protein pre A; Reference number: A29787; MUID:87280213; PMID:3611107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-140, R', 142-359, RAG', 363-371, P', 373-508 «CHE»
A; Cross-references: GB:J02783; NID:g339646; PIDN:AAA61169.1; PID:g339647
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Pihlajaniemi, T.; Helaakoski, T.; Tasanen, K.; Myllyla, R.; Huhtala, M.L.; Koivu, J.;
EMBO J. 6, 643-649, 1987
A; Title: Molecular cloning of the beta-subunit of human prolyl 4-hydroxylase. This subun
A; Reference number: A26632; MUID:87218523; PMID:3034602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-9, PwX', 13-43, PP', 46-48, H', 50-438, G', 440-443, G', 445-480, V', 482-508 <B
A; Cross-references: EMBL:X05130, NID:395654; PIDN:CAA2875.1; PID:335655
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Tasanen, K.; Oikarinen, J.; Kivirikko, K.I.; Pihlajaniemi, T.
J; Biol. Chem. 267, 11513-11519, 1992
A; Title: Promoter of the gene for the multifunctional protein disulfide isomerase polype
A; Reference number: A42791; MUID:92283868; PMID:1597478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Lype: DNA
A; Residues: 1-25 < TA3.
A; Cross-reterences: GB:S37207; NID:g249922; PIDN:AAB22262.1; PID:g249923
A; Note: sequence extracted from NCBI backbone (NCBIN:104755; NCBIP:104756)
R; Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
B:ectrophoresis 11, 883-891, 1990
A; Title: Development of a database of amino acid sequences for human colon carcinoma pro
A; Reference number: A33178; MUID:91176935; PMID:2079031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein

A, Molecule type: protein

R, Residues: 18-24, 'X', 26 < WAR>
R, Residues: 18-24, 'X', 26 < WAR>
R, Residues: 18-24, 'X', 26 < WAR>
B, RS Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C
Electrophoresis 11, 528-536, 1990
Electrophoresis 11, 528-536, 1990
A, Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencin A, Reference number: A61002; MUID:91031404; PMID:1699755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 17q25-17q25
A;Introns: 49/1; 118/1; 162/3; 208/3; 243/3; 285/3; 352/3; 393/1; 453/3; 482/3
C;Complex: in procollagen-proline dioxygenase forms a heterotetramer of two alpha chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Pathway: collagen synthesis
C;Function: <TD1>
A;Description: as thyroxine deiodinase (EC 3.8.1.4) reduces iodinated thyronine residues
A;Description: as thyroxine deiodinase (EC 3.8.1.4) reduces iodinated thyronine residues
C;Superfamily: protein disulfide-isomerase; thioredoxin homology
C;Keywords: ascorbic acid; duplication; endoplasmic reticulum; homodimer; intramolecular
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-508/Product: protein disulfide-isomerase #status predicted <MAT>
F;32-119/Domain: thioredoxin homology <TX1>
F;35-508/Domain: thioredoxin homology <TX2>
F;55-508/Region: endoplasmic reticulum retention signal
F;53-56,397-400/Disulfide bonds: redox-active #status predicted
                                                                                                       (prot
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R;Morris, J.I.; varanuanis, ....
Biochim. Biophys. Acta 949, 169-180, 1988
A;Title: Characterization of a cDNA for human glutathione-insulin transhydrogenase
A;Reference number: A30055; MUID:88134925; PMID:3342239
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Residues: 317-326,351-363,'X',365-370,402-406,'X',408-419 <BAU>
                                                                                                                                                                                                                                  A;MOlecule type: mRNA
A;Residues: 293-351, R',353-401,'HS',404-459,'Q',461-508
A;Cross-references: EMBL:X07077
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A,Cross-references: GDB:120708; OMIM:176790
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Gaps

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Gaps

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Indels

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RESULT 15
S6672
Shosphatidylinositol-specific phospholipase C - northern European squid
C;Species: Loligo forbesi (northern European equid)
C;Species: Loligo forbesi (northern European equid)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S66672; S74310; S41169
R;Carne, A.; McGregor, R.A.; Bhatia, J.; Sivaprasadarao, A.; Keen, J.N.; Davies, A.; Firr FBBS Lect. 372, 243-248, 1995
A;Title: A beta-subclass phosphatidylinositol-specific phospholipase C from squid (Lolig A;Reference number: S66672; MUID: 96000215; PMID: 7556677
A;Accession: S66672
A;Molecule type: mRNA
A;Residues: 1-875 <CAR>A;Accession: S6672
A;Molecule type: mRNA
A;Cross-references: UNIPROT: Q25285; EMBL: X76968; NID: 9439518; PIDN: CAA54275.1; PID: 94395
A;Accession: S74310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 90-102;278-297,756-770 <CAN>
A; Residues: 90-102;278-297,756-770 <CAN>
A; Residues: 90-102;278-297,756-770 <CAN>
A; Residues: 90-102;278-297,756-770 <AN>
CANDEL TO Thosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homplogy
P; 325-471/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homplogy
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Pred. No. 88;
2; Mismatches 0; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative
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805 GGAADDDDL 813
2 GGSCDDDDL 10
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Search completed: May 27, 2005, 13:48:41 Job time : 3.92111 secs

|:||||:|| 476 GAGDDDELA 484

8 8

3 GSGDDDDLA 11

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 27, 2005, 13:35:35 ; Search time 0.921109 Seconds (without alignments) 972.511 Million cell updates/sec

US-10-622-893A-1 63 Title:

1 MGGSGDDDDLAL 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Segmence 20812. A				27609,	3384, A	22504,	25952,	11598,		3, 2	30,	29,	Sequence 29, Appl	28,	36,	N	36,	2798	26,	26,	1,7	37,	37,	3, 2	12	
Olimanis	US-09-248-796A-20812	US-09-248-796A-19565	-00-	US-09-270-767-54420	-60-	US-09-540-236-3384	US-09-248-796A-22504	US-09-252-991A-25952	US-09-949-016-11598	US-09-252-991A-30715	US-07-872-673B-3	US-09-807-258-30	US-08-557-122A-29	US-09-262-666-29	US-08-557-122A-28	US-08-557-122A-36	US-09-262-666-28	US-09-262-666-36	US-09-252-991A-27987	US-08-557-122A-26	US-09-262-666-26	US-08-969-334-1	US-08-200-900A-37	US-08-794-042-37	US-09-217-228-3	US-09-902-540-15731	US-09-217-228-5
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Length	265	408	151	151	264	409	543	1138	390	445	491	508	509	509	510	510	510	510	675	3052	3052	10	11	11	23	106	114
% Query Match	69.8	68.3	66.7	66.7	66.7	66.7	66.7	66.7	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	65.1	63.5	63.5	63.5	63.5	•	63.5
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Result No.	-	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

TYPE: PRT

Appli	App	App	App	App	App	App	App	App	App	App	App	App	ppli	1, A	Appli	Appli	Appl
5, A	383,	383,	383,		383,	383,	383,		846,	846,	846,	846,	6, App	14651	2, A	2, A	14,
Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Segnence
US-09-272-342B-5	US-09-439-313-383	US-09-352-616A-383	US-09-636-215-383	US-09-685-166A-383	US-09-679-426-383	US-09-759-143-383	US-09-651-236-383	US-09-636-215-846	US-09-685-166A-846	US-09-679-426-846	US-09-759-143-846	US-09-651-236-846	US-09-272-342B-6	US-09-248-796A-14651	US-09-328-869-2	US-09-629-774A-2	US-07-745-382-14
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134	154	154	154	154	154	154	154	161	161	161	161	161	177	290	291	291	296
63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
8	67	30	31	32	33	34	35	36	37	38	39	9	-	2	13	44	ī,

ALIGNMENTS

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Sequence 20812, Application US/09248796A
Sequence 20812, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
FILE REPRENCE: 107196-1122
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1999-02-13
FRIOR PEPLICATION NUMBER: US 60/074,725
FRIOR PEPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
LENGTH: 265
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Sequence 19565, Application US/09248796A

Sequence 19565, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WINBER: US/09/248,796A

CURRENT PEDLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PELING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

LENGTH: 408
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Pred. No. 16;
1; Mismatches 1; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Candida albicans
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SEQ ID NO 3384
LENGTH: 409
TYPE: PRT
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Facent No. 670341
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54420
LENGTH: 151
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT PELLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39203
LENGTH: 151
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                                                     Score 43; DB 4; Length 408;
Pred. No. 35;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 42; DB 4; Length 151; 87.5%; Pred. No. 18; 1: Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-54420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27609, Application US/09248796A
                                                                                                                                                                                                                           RESULT 3
US-09-270-767-39203
Sequence 39203, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                     Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
; ORGANISM: Candida albicans
US-09-248-796A-19565
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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US-09-248-796A-27609
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US-09-270-767-54420
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANK

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 27609

LENGTH: 264
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US-09-540-236-3384
US-09-540-236-3384
US-09-540-236-3384
US-09-540-236-3384
US-08-2384
US-08-2884
US-08-2885
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Referent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WINDER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
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Pred. No. 32;
0; Mismatches 1; Indels
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0; Mismatches
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Best Local Similarity 87.5%;
Matches 7; Conservative
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US-09-248-796A-27609
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Best Local Similarity 97.5
Matches 7; Conservative
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US-09-540-236-3384
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COMPUTER READABLE FORM:
MEDIUM TYPE: Type 2DD, 3.50 inch, 720 KB
COMPUTER: Apple Macintosh SE
COMPUTER: Apple Macintosh SE
COMPUTER: Apple DOS
SOFTWARE: Microsoft Word Version 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,673B
FILING DATE: 19220417
CLASSIFICATION: 435
PRIOR APPLICATION TATA:
APPLICATION NUMBER: Japanese Patent Application No. 5578466. 114074/91 and 31160
FILING DATE: 18-APR-1991 and 30-OCT-1991
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   Sequence 30715, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT PILIDING DATE: 1999-02-18
FRICK FILING DATE: 1998-02-18
FRICK FILING DATE: 1998-02-18
FRICK PAPLICATION NUMBER: US 60/074,788
FRICK PAPLICATION NUMBER: US 60/094,190
FRICK PILING DATE: 1998-02-18
FRICK PILING DATE: 1998-02-18
FRICK PILING DATE: 1998-02-18
FRICK FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/07872673B
Patent No. 5578466
GENERAL INFORMATION: Setsuko KATO, No. 5578466uhiro TAKAHASHI, and Masanor TITLE OF INVENTION: Co-expression System of Protein Disulfide Isomerase Gene an NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: ADDRESSE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS & CUSHWAN STREET: 130 WATER STREET
CITY: BASSACHUSETTS
COUNTRY: US
COUNTRY: US
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Pred. No. 79;
3; Mismatches 2; Indels
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ORGANISM: Pseudomonas aeruginosa
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190 LAGSGADDDIAV 201
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                     359 GAGDDDDL 366
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                                                                                                                                                                                                  JS-09-252-991A-30715
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US-07-872-673B-3
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### Sequence 25952, Application US/09252991A

### Sequence 25952, Application US/09252991A

### Patent No. 6551795

### CENERAL INFORMATION:

### APPLICANT: Marc J. Rubenfield et al.

### TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

### TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

### TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

### TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

### CURRENT APPLICATION NUMBER: US 60/074,788

### PRIOR FILING DATE: 1999-02-18

### PRIOR PLICATION NUMBER: US 60/094,190

### PRIOR PLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11598, Application US/09949016
; Sequence 11598, Application US/09949016
; Batent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYWORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOOU3307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR PAPLICATION NUMBER: 60/237,768
; PRIOR PAPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR PAPLICATION NUMBER: 60/231,498
; RIOR APPLICATION NUMBER: 60/231,498
; PRIOR SEQ ID NOS: 207012
; SOCTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11598
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                                                                                                                               DB 4; Length 543;
68;
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                                                                                                                               Score 42; DB 4; Pred. No. 68; 0; Mismatches
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                                                                                                                               66.78;
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22504
                                                                                                                                                             Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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298 GGGDDDD 305
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Best Local Similarity
Matches 7; Conserv
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ORGANISM: Human
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TOPOLOGY: linear MOLECULE TYPE: peptide
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US-08-557-122A-29
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US-09-262-666-29
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US-08-557-122A-29
US-08-557-122A-29
Sequence 29, Application US/08557122A
Sequence 29, Application US/08557122A
GENERAL INFORMATION:
APPLICANT Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58796640 No. 5879664th America, Inc.
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                       Gaps
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Fatent No. 6670166
GENERAL INFORMATION:
FAPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/807,258
CURRENT APPLICATION NUMBER: 2001-06-11
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
SEQ ID NO 30
FENDER FILING DATE: 1999-10-15
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.1%; Score 41; DB 4; Length 508; 87.5%; Pred. No. 91;
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                       0; Indels
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COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
  Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGIGTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
Best Local Similarity 87.5%;
Matches 7; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                   460 GAGDDDDL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-807-258-30
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477 GAGDDDDL 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GSGDDDDL 10
                                                            3 GSGDDDDL 10
                                                                                                                                                             RESULT 12
US-09-807-258-30
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Patent No. 6346244
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63462440 No. 6346244disk of No. 6346244th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                    Gaps
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Score 41; DB 2; Length 509;
Pred. No. 91;
1; Mismatches 0; Indels
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US-08-557-122A-28
i Sequence 28, Application US/08557122A
j Patent No. 5879664
j GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Mailand
i TITLE OF INFORTION:
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 3980.204-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 TELEPHONE: 212-878-9655 INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,122
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Lambiris, Blias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    Query Match 65.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Matches 7; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
CITY:
New York
CITY:
New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER: Plopy disk
COMPUTER: READABLE PORM:
COMPUTER: Plopy disk
COMPUTER: TEMP C COMPATIBLE
COMPUTER: TEMP C COMPATIBLE
COMPUTER: TEMP C COMPATIBLE
COMPUTER: TIMP C COMPATIBLE
COMPUTER: 11-DEC-1995
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 102/08/557,122A
FILING DATE: 11-DEC-1995
CLASSITICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGENANICATION INFORMATION:
NAME: 212-67-0123
TELEPHONE: 212-67-0123
TELEPHONE: 212-67-0123
TELEPHONE: SEQUENCE: ASSENDENCE: ASSEN
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Search completed: May 27, 2005, 13:49:57 Job time : 1.92111 secs

3 GSGDDDL 10 |:|||||| 479 GAGDDDDL 486

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27, 2005, 13:28:55; Search time 95.9723 Seconds (without alignments) 2331.700 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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10
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US-10-622-893A-3 Perfect score:

2329 1 AVTKSSSLLIVGAGTWGTST......MDFHDVKEWTNVQYRDISKL Sequence:

437

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 DB seq] DB seq ; Minimum I Maximum I

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB
85.1 437 2
1242 53.3 445 2 042629 848 36 4 426 2 068280
36.3 418 2
28.3 437 2 (
27.0 438 2 (
26.8
43/ 2 Q/63A6 488 5 21 0 412 2 Q43D29
20.0 433 2
18.3
16.6
16.2 486 2 (
15.1 446 2 (
14.9 435 2
8.2 390 1
7.9 387 2
371 2 (
7.8 440 2
181 7.8 384 1 MSOX STRAW
7 6 390 1
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371 2
174 7.5 371 2 Q81PTZ
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367 2 (
7.3 773 2 (
170 7.3 371 2 Q81CN0
7.3

Q95u69 drosophila P79371 oryctolagus P40873 arthrobacte			Q8empO oceanobacil P23342 bacillus sp Q8fei5 escherichia
Q95U69 SOX RABIT MSOX ARTST	Q8XT <u>7</u> 8 Q88GE9 Q8N6Z6	YGCN RCOLI Q82M71 Q89M92 Q685L2	QBEMPO MSOX_BACSN QBFBIS
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399 390 388	382	381 381 331	375 387 433
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170 169.5 166	166 165 162.5	160 159.5 159.5 155	155 155 153
33	36	3 6 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 E 4 7

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                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fructosyl amine: oxygen oxidoreductase.
Appergillus tumigatus (Sartorya funigata).
Ekkaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NGI_TAXID=5085;
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100.0%; Pred. No. 1.9e-174;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 437; Conservative
                                                           PRELIMINARY;
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RESULT 1
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Query Match
Best Local 9
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  ASGRGFKYLPSIGNLIVDAMEGKVPOKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=33178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48869 MW; B838EA0AB2105E36 CRC64;
                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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82.6%; Pred. No. 3.8e-147;
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                                                                                                                                                                                                                             437
                                                                                                                                                                                                                                                                      Created)
                                                                                 HDVKEWTNVQYRDISKL 437
                                                                                                                      422 HDVKEWTNVQYRDISKL 438
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EVKEWTNVTQRDISKL 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 360; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 EDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 KFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSAD--GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 SLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Fructosyl amine:oxygen oxidoxeductase.
Aspergillus fumigatus (Sartorya fumigata).
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TAXID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=DEHA0A01157g;
Debaryomyces hansenii CBS767,
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Sacharomycetacee; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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BEQUENCE FROM N.A.

Takahashi M., Pischetsrieder M., Thein M., Roth J.C., Monnier V Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AF035700; AAB88209.1; -..

EMSL, AF035700; AAB8209.1; -..

InterPro; IPR006076; Fad oxred.

InterPro; IPR000505; NAD BS.

InterPro; IPR000584; ThiF_domain.

Pfam; PF01266; DAO; 49364 NW; 57685EE6CA535B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 445;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
55-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|P78573 Aspergillus fumigatus Fructosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 53.3%; Score 1242; DB 2; al Similarity 52.1%; Pred. No. 5.1e-89; 228; Conservative 78; Mismatrher 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 PNRVMDFHDVKE--WTNV 429
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PRELIMINARY;
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                                                                                                                 Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
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InterPro; IPR006076; Pad_oxred.
InterPro; IPR000205; NAD_BS.
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RYGGSNEVKDLKNVKQWSN
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                                              SEQUENCE PROM N.A STRAIN=CBS767;
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RESULT 5 Q6BZA7 ID Q6BZA7 AC Q6BZA7;

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A defontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
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A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T., "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN---L 120
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                                                                                                                                                                                                       Debaryomyces hansenii CBS767.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|Q92204 Aspergillus terreus Fructosyl amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
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SEQUENCE 418 AA; 47714 MW; 448BCEF20CEB486A CRC64;
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42.0%; Pred. No. 5.7e-58;
tive 71; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CR382133; CAG84414.1; -. InterPro; IPR006076; Fad_oxred.InterPro; IPR000205; NAD_BS.
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les 181, Conservative
                                                                                                                                                                       ORFNames=DEHA0A03223g;
Debaryomyces hansenii
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=284592;
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"The veA gene is necessary for the inducible expression by fructosyl amines of the Aspergillus nidulans faoA gene encoding fructosyl amino acid oxidase (amadoriase, EC 1.5.3).";
Arch. Microbiol. 178:344-350(2002).
                          Name=faoA;
Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                        STRAIN=FGSC A4;
BIDLINES-2261769; PubMed=12375102;
Jeong H-Y., Song M.H., Back J.H., Han D.M., Wu X., Monnier Jahng K.Y., Chae K.S.;
  Fructosyl amino acid oxidase
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                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 -----VELTRPEOFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GLEKTNIWLESEDDILAKAPH-FTREQIKGWKGLFCGDG-GWLAAAKAINAIGTFLKSQG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 VKFGFGSAGTFKRPLFAPDGATCS------GVETVDGTKYFADKVVLAAGAWSSTLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 DLEDQCVSKAWVFAHIQLTPQESAQYKDVPVVVDGDYGFFFEPN-EHGVIKVCDEFPGFS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 NM-----VQSADGTMMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARIC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 RFKLHQPYGATSPKLISVPRSHAKHPTDTYPDSSEETIRKAIARFMPRFKDKELFNRSMC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 394
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SEQUENCE FROM N.A.

MEDLINE=97175014; PubMed=9022674;

MEDLINE=97175014; PubMed=9022674;

Yoshida N., Sakai Y., Isogai A., Fukuya H., Yagi M., Tani Y., Kato N.;

Yoshida N., Sakai Y., Isogai A., Fukuya H., Yagi M., Tani Y., Kato N.;

Primary structures of fungal fructosyl amino acid oxidases important for measurement of glycated proteins.";

Eur. J. Biochem. 242:499-705(1996).

Embl. Y09021; CAA70219.1; -.

Pfam; PF01266; DAO; 19.1; -.

Pfam; PF01266; DAO; 18.31 MW; E681B8702DE4A574 CRC64;

SEOUENCE 437 AA; 48231 MW; E681B8702DE4A574 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 RNGPDLQ----LSLEALDMWKNDPLFKPFFHNVGMLDCSSSQEGIASLRRKHQDLIDANI
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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Last annotation update)
                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        Penicillium janthinellum (Penicillium vitale).
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Matches 156; Conservative
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416 RVMDFHDVKEW 426
                                                  407 HVKDLKDIKDW 417
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5079;
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Q96UT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 LVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 NFMLESEDEILAKAPH-FTQEQIKGWKGLFCGDG-GWLAAARAINAIGQFLKEQGVKFGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 FAHIQLTPAEAAAXKNTPVIYDGDYGFFFEPN-ENGIIKVCDEFPGFTHFKMHQPYGSPA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 PKPISVPRSHAKHPTDTYPHASEVTIKKAINRFLPRFNDKELFNRAMCWCTDTADANLLV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 CEHPRWKGFYLATGDSGHSFKLLPNIGKHVVELLEERLESVFKDAWRWRPGSGDALKSRR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                          10 IVVGGGGTMGSSTALHLLRAGYTPSNITVLDTCPIPSAQSAGYDLNKIMSI--RLRNKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-GAGTFKKPLFADAHEKTCIGVETVDGTKYYADKVVLAAGAWSSTLVDLEEQCVSKAWV
                                                                                                                                                                                                                                                                                                                                                                                                          8 LLIVGAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 GTPQGRVVTLIFENNDVK---GAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 LVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQ----SAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 GTMMSIPFEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWCADTANREFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 DRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNP-----
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                  Length 438;
                                                                                                                                                                                                                                                                            27.0%; Score 629; DB 2; Length 43 34.0%; Pred. No. 7.5e-41; cive 73; Mismatches 168; Indels
Jeong H.-Y., Song M.H., Back J.H., Han D.M., Monnier V.M
Jahng K.-Y., Chae K.-S.,
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF416568, AAL09028.1; -
                                                                                                                                                                              PFam; PF01266; DAO; 1.
SEQUENCE 438 AA; 48433 MW; BF72BC2CC4D57316 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Fructosyl peptide oxidase (EC 1.5.3.-).
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                                                                                                                    InterPro; IPR006076; Fad oxred.
InterPro; IPR000205; NAD_BS.
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.0%
Matches 148; Conservative
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STRAIN-NISL 9330;
                                                                                                                  Local Simi
hes 141;
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                                                                                                                                                                                                                                                                                                            ----GEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREA 170
                                                                                                                                                                                                                                                                                                                                                 QRMGVKFVTGTPQGRVVTLIF--ENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKN 228
                                                                                                                                                                                                                                                                                                                                                                                                                         ---VQSADGTWMSIPFEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWCAD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSOEGLDRLGVRVRP-- 114
                                                                                                                                                                                                                                                                                                                              116 DAGIGLEKTNVWLESEDEILAKAP-NFTREQVKGWKGLFCTDG-GWLAAAKAINAIGIFL 173
                                                                                                                                                                                                                                                                                                                                                                                     QLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIXICDEHPGYTNM-- 286
                                                                                                                                                                                                                                                                                                                                                                                               292 HQPYCAASPKMISVPRSHAKHPTDTYPDASEVTIRKAIARFLPEFKDKELFNRTMCWCTD 351
                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                              1 AVTKSSSLLIV--GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISS
                                                                                           oxidases
                                                                                                                                                                                                                  Gaps
                                                           Eukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Coniochaetales, Coniochaeta
                                                                                                                                                                                                                  40;
                 Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Eupenicillium.
NCBI TaxID=69803;
                                                                                                                                                                                               Length 437;
                                                                                                                                                                                             26.8%; Score 625; DB 2; Length 43
34.2%; Pred. No. 1.5e-40;
ive 81; Mismatches 174; Indels
                                                                                                                                                                            437 AA; 48187 MW; A79159C804B63848 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AANRNWRDTLGRFGGPNRVMDFHDVKEW 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
         Supenicillium terrenum.
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=227947;
                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                   Oxidoreductase
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                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 HIQLTPEEAAEYKGVPVVYNGEFGFFFEPN-EFGVIKVCDEFPGFSRFKEHQPYGAPSPK 301
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                                                                                                                                                                                                                                                                                                                                                                                 68
MEDLINE=22937253; PubMed=14575701; DOI=10.1016/j.bbrc.2003.09.169; Hirokawa K., Gomi K., Kajiyama N.; Molecular cloning and expression of novel fructosyl peptide oxidases molecular application the measurement of glycated protein."; Blochem. Biophys. Res. Commun. 311:104-111(2003).

EMBL; AB116147; BAD00186.1; -. InterPro; IPR006076; Pad oxred.

InterPro; IPR000205; NAD_BS.

Pfam; PF01266; DAO; I. A.

SRQUENCE 437 AA; 48634 MW; 5702BCFFD1C2D979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 IEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL-VELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R---PEOFRKLAPEGVLOGD-FPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TPQGRVVTLIFENNDVK--GAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQ-----SADGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMSIPFEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDR
                                                                                                                                                                                                                                                                                                                                        8 LLIVGAGTWGTSTALHLARRGY - - TNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
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                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                  Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                              25.8%; Score 600; DB 2; Length 43 32.7%; Pred. No. 1.4e-38; tive 86; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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                                                                                                                                                                                                                                                                     ilarity 32.7%;
Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DIAANRNWR 405
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NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
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A James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitech E., Sketcon J., Simmonds M., Squares D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreals E., Rieger M., Schafer M., Muller-Auer S., Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 YHPDYENLFVCTGGSGHGFKFFFILGKYSIGCMFRELEEPLLKKWRWKKENLEFPAALDHS 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 PGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL-DFKNQLRP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 TMMSIPFEKTOI----PKEAETRVRALLKETM-PQLADRPFSFARICWCADTANREFLID 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 NYDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSA------CSQEGLDRLGVRVR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 GVSFISG-PEGTVEELITEENVVKGVRTTTG-AYMAEKLIFATGAWTASLLPNDHTRFLA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHPOYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPOKIHELIKW---NPDIAANRNW 404
                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADG
                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                             21.0%; Score 488.5; DB 2; Length 412; 30.1%; Pred. No. 7.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                       78; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                    46319 MW; BD36B86075D3F4EF CRC64;
                                                                                                                                                                                                                                                                                                GeneDB SPombe; SPBC354.15; -.
InterPro; IPR006076; Fad oxred.
InterPro; IPR000205; NAD_BS.
                                                                                                                                                                                                                                                         Nature 415:871-880(2002).
EMBL; AL022071; CAA17815.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches 130; Conservative
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Q9UTM9
ID Q9UTM
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OSUTM9; 01-MAY-2000 (TrEMBLrel 01-MAY-2000 (TrEMBLrel 01-MAR-2004 (TrEMBLrel SPAC139.04c protein.

PRELIMINARY;

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MEDINE-ZIRAGAGI, PUDMEGLIBSD350, DOI=101038/NATURE/CASA

WOOD V., GWilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
By Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
A James K., O'Neil S., Raunders D., Squares S., McDonald S., McLean J.,
A Noney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A Diver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Richerford K., Rutter S., Saunders B., Seger K., Sharp S.,
Skelton J., Simmonds M., Squares S., Stevens K.,
A Skelton J., Simmonds M., Squares S., Stevens K.,
A Skelton J., Simmonds M., Squares S., Stevens K.,
A Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
A Meltjens I., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
A Doll T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
A Goffeau A., Cadieu E., Dreano S., Gloux S., Lehrach H., Morter S.,
A Loas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
A Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
A Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
A Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thore Centti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L.,
Cerutti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L.,
A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
A Rhakovski G.V., Ussery D., Barrell B.G., Nurse P.;
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EMBL, Ali32667; CABS9618.1; --
PIR; T37605; T37605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 SSSLLIVGAGTWGTSTALHLAR-RGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
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                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
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InterPro; IPR006076; Fad_oxred.
InterPro; IPR0060583; GATase_2.
Pfam; PF01266; DAO; 1..
PROSITE; PS00443; GATASE TYPE II; UNKNOWN 1.
SEQUENCE 433 AA; 48973 MW; 170081BB3D48B1BE CRC64;
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                            Schizosaccharomyces
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=972h-;
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InterPro; IPR006076; Fad_oxred
InterPro; IPR000205; NAD_BS.
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SEQUENCE 433 AA; 48
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                                                                         GVRVRPG-
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Q6CLIO;
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A Galagan J.E., Ealvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
B Eltins T., Engels R., Wan E.-J., Smirnov S., Purcell S., Rehman B.,
B D. D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metracherg R.L., Perkins D.D., Kroken S.,
A Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Rafford A., Aramayo R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
"The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
                            PGYTNMVQS---ADGTMMSIPF---EKTQIPKEAETRVRALLIKETMPQLADRPFSFARIC 334
                                                                                              WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-07-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Related to fructosyl amino acid oxidase)
Name=NCU04771.1; Synonyms=B15B10.150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%; Score 426.5; DB 2; Length 502; 29.2%; Pred. No. 7.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Neurospora genome project;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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502 AA; 52930 MW; 39748F9E553D4FDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                       502 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                            395 NPDIAANR-NWR 405
                                                                                                                                                                                                                                             405 REDDKASELKWR 416
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SSGQYSNNKDEIEVNEILAEEAFNGWK-----NDPLFKPYYHDTGLLMSACSQEG-LDRL 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QIPKEAETRVRALLKE--TMPQLADRPFSFARICWCADTANREFLIDRHPQYH 353
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaaten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Kosul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
I "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                  --GSSGSW-GYI-NGLSGWANAGASMAWLYKRVRAEGRINFVA----GEVTNLEVSGNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 GTPVAPGTSVIDKSKLTGMDYARFSWANVLSLASSDPELAARIKECPNTDAIKAALGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                   197 KGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVI
                                                                                                                                        ----EDPNLV----ELTRPEQFRKLAPEGV
                                                                                                                                                                                                                                                                              138 LQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG-VKFVTGTPQGRVVTLIFENNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 SLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWR 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 GLFVATGDSGHAFKFLPVIGEKIADVIAGQCP-------PEFVGKWNWR 464
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|Q9UTM9 Schizosaccharomyces pombe Putative fructosyl
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Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382126; CAG97917.1; -
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SEQUENCE FROM N.A.
                STRAIN=CBS767;
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Amennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zenlou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Anicker P., Souciet J.L.;
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
                                                                                                                                                                                                                      112 LQLLQ-TKFNKCKTVELHKELTCGGKFP----QFSHSQRYDEIRYNPDCGIGLARDSLVT 166
                                                                                                                                                                                                                                                                                            167 MKNYAESLGV------VFHEND--GAVSVSAGTVQCESGRKFLGHKIIVACG 210
                                                                                                                                                                                                                                                                                                                                                          211 ANTVSLLPMYGÓIRATGLYVGHIQLTDKEYQKLKDIPVVFNSSLGYLFPPDKHTRILKÍC 270
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                                                                                                                                        VNEIILAEBAFNGWKNDP-----LFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL 120
                                                                                                                                                                                                      VELTRPEQFRK-----LAPEGVLQGDFPGWKGYFARS------GAGWAHARNALVA 165
                                                                                                                                                                                                                                                                                                                              218 ASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKIC 277
                                                                                                                                                                                                                                                                                                                                                                                          278 -DEHPGYTNMVQSADGTMMSI-PFEKTQIPKEAETRVRALLKETMPQLAD-----RP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 FSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKV-PQ 386
                                                                                                                                                                     VYAALAVEAMGYWHGESDKFLPRGMLHDCYSHCGRL-SAIQDKNTSRYAF-----DNDS 111
                                                                          67
                                                                                                        28
                                                                                              166 AAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVT-----GDGKIWRAERTFLCAG
                                                                         LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|P78573 Aspergillus fumigatus Fructosyl amine: oxygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNAMES=DEHA0F00528g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                             82;
             Length 433;
             Query Match 16.6%; Score 386; DB 2; Length 43
Best Local Similarity 28.3%; Pred. No. 9.2e-22;
Matches 125; Conservative 67; Mismatches 167; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 KIHELIKWNPDIAANRNWRDT 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 FRA-QYAEKKHYQE----LAFRAFEIWQEWDRKIQLLPESEVKEF----TGLRLLDLCGML 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ---SQEGLDRLGVR----VRPGEDPNLVELTRPEQFRKLAPEGV------LQGDFPGW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 KKHEAELVVINCGPWSTSLVPELDGINEGTGGNILICKIPDSRKDLKVKYSSKNFPII-G 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 WKSGHSREHDYLAGMFIFPVIEPEGILKIIVRQTKYTNPEKLANGRVVSIPKTSNSNPPF 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 KGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVT-LIFENNDVKGAVTGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 IERG------FFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSI-----PF
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr[043029 Schizosaccharomyces pombe Putative fructosyl amino acid oxidase.
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Debaryowyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 486;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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55220 MW; 5861D01F87F8C830 CRC64;
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16.2%; Score 376.5; DB 2;
Best Local Similarity 29.1%; Pred. No. 5.9e-21;
Matches 129; Conservative 59; Mismatches 181;
                                       EMBL; CR382138; CAG88679.1; -...
GO; GO:0003824; F:catalyric activity; IEA.
InterPro; IPR000676; Fad_oxred.
InterPro; IPR000205; NAD BS.
InterPro; IPR000205; NAD BS.
InterPro; IPR000594; Reg_chr_condens.
InterPro; IPR000594; ThiF_domain.
Pfam; FF012665; DAO; 1.
PROSITE; PS00628; RCC1 2; UNKNOWN 1.
SEQUENCE 486 AA; 55220 MW; 5861D01F87FBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGL------LMSACSQEGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRLGVRVRPGEDPNLVELTRPEQ-FRKL---APEGVLQGDFPG---W-KGYPARSGAGWA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HARNAL---VAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKICDEHPGYTNMVQ-----SADGTMMSIPFEKTQIPKEAETRVRALLKET 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KVNEREEGKMDYYDSAEDVFRSIHNRSPNSVETTELGGPKKWNKGYTNRVN-GFI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 DARASIKVYYERARNPPNVNFRF----QEVEKIDYFKNTKKVKGVLLKNGDKISADLVIV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGF-FFEPDEERGE 273
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Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hannequin C., Jauniaux N., Joyer P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Zeniou-Meyer M., Ziavanovic I., Bolocin-Pukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                 Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR006076; Pad oxred.
InterPro; IPR00505; NAD—BS.
Pfam; PF01266; DAO; 1.
SEQUENCE 446 AA; 50897 MW; 6C89A7DBBAB75C6B CRC64;
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Matches 126; Conservative
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Search completed: May 27, 2005, 13:47:27 Job time: 98.9723 secs

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Best Local Similarity 82.6%; Pred. No. 1.4e-200;
Matches 360; Conservative 43; Mismatches 32;
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Sequence 3, Appli
Sequence 112, Appli
Sequence 10219, A
Sequence 21043, A
Sequence 21423, A
Sequence 24053, A
Sequence 24053, A
Sequence 12890, A
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 6873, Ap
Sequence 6873, Ap
Sequence 7499, Ap
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                                                                                                                                                                                                                                                                                                                1 AVTKSSSLLIVGAGTWGTST.......MDFHDVKEWTNVQYRDISKL 437
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep;*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep;*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep;*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-457-302-1

US-09-949-016-10219

US-09-252-991A-21043

US-09-252-991A-21423

US-09-252-991A-24053

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US-09-489-039A-12890

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US-09-31-61A-7499

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US-09-31-61A-748-5

US-09-31-61A-748-6

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Sequence 27656, A Sequence 12, Appl Sequence 80, Appl Sequence 246, Appl Sequence 17272, A Sequence 17272, A Sequence 135, Appl Sequence 14124, A Sequence 14124, A Sequence 18753, A Sequence 18753, A Sequence 8195, A Sequence 8195, A Sequence 20386, A Sequence 203		1D	
28 101.5 4.4 477 4 US-09-252-991A-27656 29 100.5 4.3 443 4 US-09-664-405-12 30 100.5 4.3 443 4 US-09-662-12 31 100.5 4.3 443 4 US-09-662-187A-80 31 100.5 4.3 443 4 US-09-664-405-12 32 97.5 4.2 421 4 US-09-602-787A-246 33 97.5 4.2 524 3 US-08-57-210A-3 34 97 4.2 524 3 US-08-57-210A-3 35 97.5 4.2 539 3 US-08-57-210A-5 36 97 4.2 556 4 US-09-622-991A-1772 39 96.5 4.1 568 4 US-09-252-991A-24791 39 96.5 4.1 359 4 US-09-222-991A-18753 40 95.5 4.1 626 4 US-09-02-540-10385 41 95.5 4.1 642 4 US-09-126-35-5199 42 95.5 4.1 642 4 US-09-126-35-5199 43 95.5 4.1 576 4 US-09-252-991A-18753 44 95.5 4.1 576 4 US-09-252-991A-16908 45 94.5 4.1 558 4 US-09-222-991A-16908	ALIGNMENTS	on US/09031059 NOBUO YASSTYCSHI YASSTYCSHI YASSTYCSHI YASSTEWART, KOLASCH AND BIRCH RESS: 11 RESS: 14, STEWART, KOLASCH AND BIRCH RCH FORM: Compatible Compatible POEDS/NS-DOS LIN Release #1.0, Version #1.30 RDH A35 BRI ER: US/09/031,059 435 BRI ORMATION: CORMATION: 10 NO: 11 STICS: 10 A0: 12 STISS: 10 Acids d d ct relevant r Corein	Similarity 82.6%; Pred. No. 1.4e-200;
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Gaps

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Indels

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422 DVKEWTNVQYRDISKL 437
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422 EVKEWTNVTQRDISKL 437
: TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-059-3
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Matches 106; Conservative
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                                                                                                                                                                PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA 241
                                                                                                                                                                                                                             182 PQGRVITLIFENNDVKGAVTADGKIWRAEQTILCAGAAAGQFLDFKDQLRPTAWTLVHIQ 241
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                                                                                                                                                                                                                                                                                          242 LKPEERAQYKNMPVVFNIEKGFFFEPDEERGEIKICDEHPGYTNMTTGADGRVRSIPFEK 301
                                                                                                                                                                                                                                                                                                                                           TQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGA 361
                                                                                                                                                                                                                                                                                                                                                            SGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFH 421
                                                                                                                                                                                                                                                                                                                                                                                                                         362 SGRGFKYLPSIGSIIADAMEDKTPAKIHKLIRWSPEIAINRNWGDRLGRFGGPNRVMDFN 421
                                                                             62 NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLV 121
                                3 VTKSSSILIIGAGTWGCSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKIISSGQYSS 62
             VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09031059;
Patent No. 5948659;
GENERAL INFORMATION:
APPLICANT: KATO, NOBUO
APPLICANT: TANI, YASHYKII
APPLICANT: FUKUYA, HIRCHII
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 0020-4253P
TELECHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/899,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKEWTNVTQRDISKL 437
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APPLICANT: Forsyth, R. Allyn
APPLICANT: Porsyth, Razi
APPLICANT: Chisen, Kari
APPLICANT: Chisen, Kari
APPLICANT: Chisen, Kari
APPLICANT: Chisen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETC
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
                                                ij
                                                                                                                                                                                            182 PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 SGRGFKYLPSIGSIIADAMEDKTPAKIHKLIRWSPEIAINRNWGDRLGRPGGPNRVMDFN 421
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                                                                                              182 PQGRVITLIFENNDVKGAVTADGKIWRAEQTILCAGAAAGQFLDFKDQLRPTAWTLVHIQ
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  DB 2; Length 437;
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                                                Indels
Query Match 85.1%; Score 1981.5; DB 2; Best Local Similarity 82.6%; Pred. No. 1.4e-200; Matches 360; Conservative 43; Mismatches 32;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 412
LENGTH: 433
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Patent No. 6589738
GENERAL INFORMATION:
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Qy 278 DEHPGYTNNVQSADGTMMSIPPEKTQIPKEAETRVRALLKETMI	ស្ត្រស្ន	APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCI; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DE: FILE REPERENCE: CLOOL307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755	PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012	; SOFTWARE; FastSEQ for Windows Version 4.0 ; SEQ ID NO 10219 ; LENGTH: 866 ; TYPE: PRT ; ORGANISM: Human US-09-949-016-10219	Query Match 6.4%; Score 148.5; DB 4; Ler Best Local Similarity 20.9%; Pred. No. 3.3e-06; Matches 98; Conservative 73; Mismatches 176; Inc	Qy 9 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN : :	109	Qy 112 V-RPGEDPNLVELTRPEQFRICLAPEGVLQGDFPGWKGYF/ :	Qy 167 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAI	QY 224 LDFKNQLRFTAWTLVHIALKPEBRALYKNIPVIFNIE : ::	Qy 275 KICDEHPGYTNMVQSADGTMMSIPPEKTQIPKEAE"	Qy 327 PFSPARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLI ::	Qy 386 QKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDVKEWTNT 	SULT 6 -09-252-991A-21043
60 YTHALABLLPOFHLTAPLERRITHESLSLLTPDGVTT	QY	Qy 289 SADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFS 329 :	377 VDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRF 411 377 ISACQHREPQNLFPLYHHNVERSLLW-DVLQRY 368	RESULT 4 US-09-457-302-1 ; Sequence 1, Application US/09457302 ; Patent No. 6228626 ; GENERAL INFORMATION ; APPLICANT: ICHTRAWA. TOSHIO	APPLICANT: KOYAMA, Yasuji; TITLE OF INVENTION: SARCOSINE OXIDASE AND PROCESS FOR PRODUCING THE SAME; FILE REFERENCE: 081356/0139; CURRENT APPLICATION NUMBER: US/09/457,302	CURRENT FILING DATE: 1999-12-09 RARLIER APPLICATION NUMBER: JP 10-354482 RARLIER FILING DATE: 1998-12-14 NUMBER OF SEO ID NOS: II	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 1 ; IENGTH: 387 ; TYPE: PRT	<pre>Bp. 6.7%; Score 155;</pre>	7; 78;	::: : : : : : : : :		OY 122 BLTRPEQFRYLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRM 173	Qy 174 GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLR 231	Qy 232 PTAWTLVHIALKPEBRALYKNIPV-IFNIERGFFFE-PDEERGEIKIC 277 Db 215VEIPLQPYRQVVGFFECDEAKXSNNAHYPAFMVEVENGIYYGFPSFGGSGLKI- 267

OCIATED
DETECTION AND USES THEREOF indels 121; Gaps 22; TMPQLADRPFSFARICWCA 337 :: |: HAAGLTTYFHPGINLKKI 108 FPARSGAGWAHARNALVAA 166 GLLMSACSQEGLDRLGVR 111 | : | : :| GSIRLATTPVRVDEFKYQ 150 AERTFLCAG---ASAGOF 223 ----RGFFFEPDEERGEI 274 | | | : :: .RQERDGLLFGPYESQEKM 318 ETRVRALLKETMPQLADR 326 AMEMVPVLKKADIINVVNG 370 -----DVNKV 53 ATTGKTEHDI 371 AMEGKVPOKI 388 NVQYRD 433 ength 866; TTOYTE 442

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NUMBER OF SEQ ID NOS:
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US-09-252-991A-21423
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                                                                                                                               US-09-199-637A-367
                           SOFTWARE: Far
SEQ ID NO 367
LENGTH: 378
                                                                                      TYPE: PRT
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Sequence 21043, Application US/09252991A
Patent No. 6551795
GRERAL INFORMATION:
GREGAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 VRPGE--DPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAARE 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 146.5; DB 4; Length 4 Best Local Similarity 23.7%; Pred. No. 1.9e-06; Matches 98; Conservative 59; Mismatches 164; Indels
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
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Patent No. 6355411
PRERAL INFORMATION:
APPLICANT: Ausubel, Frederick
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Cao, Hui
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US-09-199-637A-367
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APPLICANT:
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Sequence 21423, Application US/09252991A

Sequence 21423, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A

FILE REFERENCE: 107196-116

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 LYWLDLDDQTEALQWARNHTRP---LKEVPIEEAYAAVPGLGAGFQRAVYMSGVANVRNP 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 --EHPGYTWWQSADGTWMSIPFEKTQIPKEAETRVRALLKETMPQLAD-----R 326
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                                                                                                                                                                                                                                                                                                                                                                                 5 SSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKD
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                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                               5.8%; Score 135.5; DB 3;
24.3%; Pred. No. 2.1e-05;
:ive 45; Mismatches 165;
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FastSEQ for Windows Version 4.0
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                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                            Best Local Similarity 24.3
Matches 102; Conservative
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Oy 331 ARICWCADTANREFLIDRHPOYHSLVLGCGASGGRCFKYLPSIGNLIVDAMEG 382	PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 SEQ ID NO 30872 LENGTH: 652 LENGTH: 652 TYPE: PRT		US-09-489-039A-12890 ; Sequence 12890, Application US/09489039A ; Patent No. 6610836 ; GENERAL INFORMATION:
Db 114AVTALAHWSQDFYPALGGRLLDETGLDPEVHTVG 147 Qy 121VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNA 162 L18 LYMLDLDDQTEALQWARKHTRPLKEVPIEEAYAVPGLGAGFQRAVYMSGVANVRNP 204 Qy 163 LVAAAREAQRWGVKFVTGTPQGRVVTLIFENNDVKGAVTGGCGTGFQRAVYMSGVANVRNP 204 163 LVAAAREAQRWGVKFVTGTPQGRVVTLIFENNDVKGAVTGGKITACAGASGG 222 164 LLKPLGLELPWYPK-GOMILAKPERALYKNIPUFNIERGFFFEPDEERGEIKICD 278 Qy 223 FLDFKNQLRFTAWTLVHALKPERRALYKNIPUFNIERGFFFEPDEERGEIKICD 278	RESULT 9 US-09-252-991A-24053 Sequence 24053, Application US/09252991A Sequence 24053, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS TITLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 24053 LENGTH: 484 TYPE: PATE CORGANISM: PSeudomonas aeruginosa US-09-252-991A-24053	Query Match 5.6%; Score 130.5; DB 4; Length 484; Best Local Similarity 22.2%; Pred. No. 0.0001; A KSSILIVGAGTWGTSTALHLARRGYTNVTVLDFYPVPSAIS. QY 4 KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDFYPVPSAIS.	OY 273 EIKICDEHPGYTNMVQSADGTWMSIPPEKTQIPKEAETRVRALLKETWPQLADRPFSF 330 : : : : : : :

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
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Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 NMLLGSAQAAHSLGVKIFESSPVVEVNYGKQVRVRTAM-----GSVKAAKLLWACD-- 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 ----KKHVGKEGLETLFKIANLGAGIIRERIRKYNIDADFVPGY---GYL--AVNORQLK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- PVPSAISAGNDVNKV
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20.9%; Pred. No. 0.00058;
tive 53; Mismatches 179; Indels 123;
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                                                                                                                                                                                                                                                                                                                                                Query Match
5.3%; Score 123.5; DB 4; Length 476;
Best Local Similarity 22.5%; Pred. No. 0.00056;
Matches 92; Conservative 48; Mismatches 148. Tanala 127
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APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Dennis J. Slamon
APPLICANT: Juliana J. Oh
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES
TITLE OF INVENTION: DASSOCIATED WITH HER-2/NEU OVEREXPRESSION
FILE REFERENCE: 304684, 405
CURRENT APPLICATION NUMBER: US/09/684, 405
PRIOR APPLICATION NUMBER: US 60/157, 923
PRIOR APPLICATION NUMBER: US 60/157, 923
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PSELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 94; Conserv
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                                                                                                                                                                                                                     SEQ ID NO 12890
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                                      64 SDVVIVGGGVLGLSVAYMLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFSLPE 123
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6 SSLLIVGAGTWGTSTALHL----ARRGYTNVTVLDPYPVPSAISAGNDVNKV--
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
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Patent No. 5463175
GENERAL INFORMATION:
APPLICANT: Rishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto CO. BB4F
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APPLICATION NUMBER: US/08/156,968
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                             GWA-----HARNALVAAAREAQR-----MGVKFVTG------TPQGRVVTLIF--- 191
                                                                                                                                                                                                                                                                                                                                                                                                                             ------ENNDVKGAVIGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTA 234
                                                                                                                                                            10 IVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDBIEVN 69
                                                                                                                                                                                                                                                70 EILAEEAFNGWKNDPLFKPYYHDTGLIMSACSQEGLDRLG-VRVRPGEDP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 5.0%; Score 116.5; DB 1; Length 431; 1 Similarity 22.7%; Pred. No. 0.0026; 94; Conservative 36; Mismatches 119; Indels 165;
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                                                                                                                                                                                  10 IAGAGIVGVCTALMLQRRGF-KVTLIDPNPPGEGASFGN------
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Patent No. 5776760

GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33

CORRESCONDENCE ADDRESS:
ADDRESSEB: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1:0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REREFENCE/DOCKET NUMBER: MOBILL 38-21 (13560) A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
: 431 amino acids
amino acid
               TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-391-339-18
                                                                                               Query Match
Best Local Similarity
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ZIP: 77210-4433
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US-08-484-274A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KSLANSLGDDIPL-----DTERGYHIVIANPEAAPRIPTTDASGK 298
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                                                                                                                                                                                                                                                                                                                                                                                                                  10 IVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIEVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REPRERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 05/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYS-
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4.9%; Score 115; DB 4; Length 505;
Best Local Similarity 21.9%; Pred. No. 0.0049;
Matches 92; Conservative 54; Mismatches 148; Indels 126; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 MMSIPFEK------TQIP--KEAE---TRVRALLKETMPQLADRPFS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 FIATPMEMGLRVAGTVEFAGLTAAPNWKRAHVLYTRARKLLPALAPASSEERYS 352
                                                                                                                              Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 IANGGEFVSARVIGFETEGRALKGITTTNG-VLAVDAAVVAAGAHS----
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                                                                                                                              5.0%; Score 116.5; DB 1; 22.7%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                          10 IAGAGIVGVCTALMLQRRGF-KVTLIDPNPPGEGASFGN-
                                                                                                                                                                                            36; Mismatches 119;
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                                                                                                                                                                                        Conservative
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                              Query Match
Best Local Similarity
Thes 94; Conserve
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	TGTPQGRVVTLIFENNDVKGAVT	269WGYAQGCQKRGVRVETYTDVTGFETSGGQVRVKTT 304	FLCAGASAGQFLDFKNQLRPTAWTLVHIALKPEERAL	305 RGDIACDTVVLAAGAWSPQVAKLADVKLPNEPHRHEILSTEPLKPFLG-PLVSVLD 359	261 RGFFFEPDEERGEIKICD-EHPGYTNWVQSADGIMMSIPFEKTQIPKEAETRVRALLK 317	360 SGLYFS-QSWRGBIVGGWGDAKEPAGLNMGSTLRFVSRFAQALM 402	WCAD-T	403 EQLPEVGHVKVLRQMAGCYDVTPDNNPILGRTPGLDNLLQMSGFVGHGFMMAPAV 457
226	153	269	213	305	261	360	318	403
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Search completed: May 27, 2005, 13:49:59 Job time: 35.5437 secs

OM protein

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Run

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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This sequence represents a novel recombinant fructosylamino acid oxidase (FADD-L) produced from eukaryotic cells integrated with an RT-FCR product encoding FADD-L derived from Aspergillus terreus GP1 (FERM P-15664). FADD-L can be used for the analysis of "Amadori" compounds
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                  Aar38078
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                                                                                                                                                                                                                                                                                                                                   Fructosylamino acid oxidase; FAOD-L; Amadori compound.
                                                                                                                                                                                                           ALIGNMENTS
                           AAW71462
ADCS9522
AACS9582
AAR79150
AAR79150
AAW71461
AAW71461
AAW53155
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                                                                                                                                                                                                                                                          AAW39253 standard; protein; 437 AA
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 WPI; 1998-172097/16.
N-PSDB; AAV09626.
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Sequence 437 AA;
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(without alignments)
1019.048 Million cell updates/sec
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                                                                                                                      1 AVTKSSSLLIVGAGTWGTST.....MDFHDVKEWTNVQYRDISKL
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Aam40278 i
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                     2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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AAY29100
AAW37141
AAW37141
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AAW69252
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AAW67397
AAR23780
ABB59342
AAM40278
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                                                                May 27, 2005, 13:28:05
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geneseqn2090s: *
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geneseqn2001s: *
geneseqn2002s: *
geneseqn2003s: *
geneseqn2003bs: *
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362 SGRGFKYLPSIGSIIADAMEDKTPAKIHKLIRWSPEIAINRNWGDRLGRFGGPNRVMDFN 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant fructosyl amino acid oxidase - useful in assays for amadori compounds, e.g. in diabetes diagnosis or food analysis.
                         3 VTKSSSILIIGAGTWGCSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKIISSGQYS
                                                                                                                                                                                                     182 PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA
                                                                                                                                                                                                                                                                                             182 PQGRVITLIFENNDVKGAVTADGKIWRAEQTILCAGAAAGQFLDFKDQLRFTAWTLVHIQ
                                                                                                                                                                                                                                                                                                                                                                                302 TQVPREAEMRVRKLLSETMPQLADRPFSFARICWCADTPNREFIIDRHPEXPSLVLGGGA
    VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                                                                         62 NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLV
                                                                                                                                                                              ELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGT
                                                                                                                                                                                                                                                                                                                                                         242 LKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSIPFEK
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422 EVKEWTNVTQRDISKL 437
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(first entry)
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06-JUL-1998
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                                                                ELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGT
                                                                                                                                                       PQGRVVTLI FENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA
                                                                                                                                                                                                                                            LKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSIPFEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terreus heat-resistant fructosyl amino acid oxidase (FAOD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29100 standard; protein; 437 AA.
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EVKEWTNVTQRDISKL
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lori compounds.
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cDNA library. The invention provides recombinant FAAO, DNA encoding the AFAO, an expression vector containing the DNA, a transformant transformed by the vector, and a method of preparing recombinant FAAO by culturing the transformant. The FAAO can be used in assays for, e.g. determination of anadori compounds such as glycated blood proteins, diagnosis and monitoring of diabetes or quality control of foods. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                               PQGRVVTL1FENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA 241
                                                                                                                                                                                                                                                                    TQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGA 361
                                                                                                                                                                                                                                                                                                      SGRGFKYLPSIGSIIADAMEDKTPAKIHKLIRWSPEIAINRNWGDRLGRFGGPNRVMDFN 421
                                                                                                                                                                                        ELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGT 181
                                                                                                                                                                                                                                                            LKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSIPFEK 301
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                                                                                                                              NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLV 121
                                                                                                                      VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                                                                                      Gaps
                                                                                                     1;
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                                                                                                     Indels
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                                                                                                     32;
                                                                                  ; Score 1976.5; DB 2; Pred. No. 3.5e-191; 44; Mismatches 32;
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Best Local Similarity 82.3%
Matches 359; Conservative
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EVKEWTNVTQRDISKL
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N-PSDB; AAV44893.
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                                                                   Sequence 437
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                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                        This sequence is the fructosylamine oxidase produced by the microbe of the invention. The microbe can produce fructosylamine oxidase with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoamino acid; glycoprotein; deoxycholic acid; deoxycholic amide; cholic acid amide ocryl glucoside; quaternary ammonium salt; quaternary ammonium salt cationic surfactant; concanavalin h; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromcoresol purple; glycation; diabetes; ascorbic acid; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                               Gaps
Substantially pure microorganism - used for producing fructosylamine
                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                           49.7%; Score 1156.5; DB 2; Length 440;
51.3%; Pred. No. 6.3e-108;
iive 75; Mismatches 130; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by ATG"
Misc-difference 396
                                                                         Claim 1; Page 11-13; 15pp; Japanese.
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                                                                                                                                                                                                                                                                                                     Best Local Similarity 51.3
Matches 223; Conservative
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The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound proportion of albumin into glycoalbumin with respect to the other albumin measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease
                                                                                                                                                                                                                                                                                                                          Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 QYTPLNTAEDFRKTMPEGILTGNFPGWKGFYKPTGSGWVHARKAMKAAFESERLGVKF1 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LTKQSQILIVGGGTWGCSTALHLARRGYTNVTVLDVNRIPSPISAGHDVNKLAGRLSTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM-MSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVIS--SGQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 440;
                                                                                                                                                                                                                                       Sumitani J, Imamura S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.7%; Score 1156.5; DB 5; Length
51.3%; Pred. No. 6.3e-108;
cive 75; Mismatches 130; Indels
 note= "Encoded by TTC"
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 63-65; 82pp; Japanese
                                                                                                                                                                                                                                         Kouzuma T, Yoshioka I, Arai M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scope of the invention
                                                                                                                                31-JAN-2001; 2001JP-00022953
16-FEB-2001; 2001JP-00039796
08-AUG-2001; 2001JP-00240002.
                                                                                                  10-JAN-2002; 2002WO-JP000721
                                                                                                                                                                                                       (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223; Conservative
                                                                                                                                                                                                                                                                       WPI; 2002-599854/64.
N-PSDB; ABK90475.
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                                 WO200261119-A1
                                                                   08-AUG-2002
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The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a 4-(2-hydroxyethyl)-1-piperazinyl group. The invention also relates to determining flycoalbumin and a protein-denaturing agent and/or a compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation proportion of albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
363 ASGDCGTGYKHITSIGKFISDCMBGTLEERFAKYWRWRPEKFTEFWGKDPLDRFGADDKI 422
                                                                                                                                                                                                                                                                                                                                                      Glycoamino acid; glycoprotein; deoxycholic acid; deoxycholic amide; cholic acid amide octyl glucoside; quaternary ammonium salt; quaternary ammonium salt cationic surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromcoresol purple; glycation; diabetes; ascorbic acid; mutant; mutein.
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                                                                                                                                                                                                ABG30784 standard; protein; 440 AA.
                                                                                                                                                                                                                                                                                                                   Fusarium oxysporum polypeptide #3.
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08-AUG-2001; 2001JP-00240002.
                                                          418 MDF--HDVKEWTNVQ 430
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                                                                                             423 MDLPKSDVEGWTNIK 437
                                                                                                                                                                                                                                                                             05-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium oxysporum.
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363 ASGDCGTGYVHITSIGKFISDCMEGTLEERFAKYWRWRPEKFTEFWGKDPLDRFGADDKI 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDF -- HDVKEWTNVQ 430
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                                                                                                                                                                                                                                                                                   NLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFV 178
                                                                                                                                                                                                                                                                                                                                                                    123 QYTPLNTAEDFRKTMPEGILTGNFPGWKGFYKPTGSGWVHARKAMKAAFESSERLGVKF1 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASGDCGTGYWHITSIGKFISDCWEGTLEERFAKYWRWRPEKFTEFWGKDPLDRFGADDKI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFEKTOIPKEAETRVRALLKETMPOLADRPFSFARICWCADTANREFLIDRHPQYHSLVL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRV 417
                                                                                                                                                                                                       acting on glycoamino acids. This sequence represents a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoamino acid, glycoprotein, deoxycholic acid, deoxycholic amide, cholic acid amide ocryl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A; betaine, ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes;
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                                                                                                       Length 440;
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                                                                                                                                             131; Indels
                                                                                                   49.4%; Score 1150.5; DB 5; 51.0%; Pred. No. 2.6e-107; ive 75; Mismatches 131;
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                                                              Sequence 440 AA;
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4-(2-hydroxyethyl)-1-piperazinyl group. The invention also relates to compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation proportion of albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease acting on glycoamino acids. This sequence represents a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycomino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a
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                                                                                                                                                                                                                                                                             Sumitani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 72-75; 82pp; Japanese.
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                                                            31-JAN-2001; 2001JP-00022953.
16-FEB-2001; 2001JP-00039796.
08-AUG-2001; 2001JP-00240002.
30-JAN-2002; 2002WO-JP000721
                                                                                                                                                                                                   (ASAH ) ASAHI KASEI KOGYO KK
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RESULT 8 ABG30783

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123 QYTPLNTAEDFRKTMPEGILTGNFPGWKGFYKPTGSGWVHARKAMKAAFEESERLGVKF1 182
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                                                                                                                                                                   SNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGED-P 118
                                                                                                                                                                                         64 SKGDDEDSIWKALSYAAAQGWLHDPVFQPFCHNTGSVVAGSTPKSIKQL-VEDBIGDDID 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fructosylamine oxidase; fructosyllysine; fructosylvaline;
Amadori compound; medical examination; diagnosis; serum glucose level;
food inspection; enzyme.
                                                                                                          NLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFV
                                                                                                                                                                                                                                                                                                                                    TGTPQGRVVTLIPENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                             243 HIQITPEETKLYKNLPPLFNINQGFFMEPDEDLHQLKMCDEHPGYCNWVEKPGSKYPQSI
                                                                                  2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVIS--SGQY
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                   4.1e-107;
  49.3%; Score 1148.5;
                   51.0%; Pred. No. 4.1e
ive 75; Mismatches
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24-OCT-2002; 2002JP-00309734.
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
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                                                                                                                                                                                                                                                                                           cholic acid amide octyl glucoside; quaternary ammonium salt; quaternary ammonium salt attoric surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes; ascorbic acid; mutant; mutein.
                                                                                                                                                                                                                                                                       deoxycholic acid; deoxycholic amide;
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246
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                                                                                                                                                                                                                                  Fusarium oxysporum polypeptide #2.
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                                                                                                    ABG30783 standard; protein; 440
                                                                                                                                                                                                                                                                         glycoprotein;
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16-FEB-2001; 2001JP-00039796
08-AUG-2001; 2001JP-00240002.
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MDLPKSDVEGWTNIK 437
                                                                                                                                                                                         (first entry)
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Fusarium proliferatum-originated fructosylamine oxidase useful in measurement of Amadori compound and particularly applicable in medical examination including diagnosis and management of diabetes.

Sequence 440 AA;

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ADE81213 standard; protein; 432
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             30-SEP-2004
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                     The invention relates to a novel fructosylamine oxidase isolated from Fusarium proliferatum. The enzyme has the following physiochemical characteristics: (a) activity against fructosyllyshine equivalent to or higher than that against fructosylvaline; (b) optimum pH for enzyme activity of 7.5; (c) enzyme stability optimally at 30-40 deg C; and (d) a molecular weight of about 39 kDa as measured by SDS-PAGE and about 39.4 kDa by gel filtration. Also disclosed is a similar Fructosylamine oxidase characterized by: (i) activity against fructosylvaline and no detectable activity against fructosylvaline mpH for enzyme activity of 7; (iii) enzyme stability optimally at 30-40 deg C; and (iv) a molecular weight of about 49 kDa as measured by SDS-PAGE and about 58 kDa by gel filtration. The oxidases are useful in the measurement of Amadori compounds and particularly applicable in medical examination including compounds and particularly applicable in medical examination including for treatment and prevention of diabetes by controlling serum glucose level for treatment and prevention of complications, and in food inspection. This sequence represents the fructosylamine oxidase designated Q2.
                                                                                                                                                                                                                                                                                                                                                                                                  QYTPLNTAEDFRRTMPBRILTGDFLGWKGFYKPRGSGWVHARKAMKAAFEESQRLGVKFI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NK--DEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGED-P 118
                                                                                                                                                                                                                                                                                                                                                                                                                                         NLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAARBAQRMGVKFV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fructosylamine oxidase; enzyme; fructosylamine; fructosyl valine.
                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                              Length 444;
                                                                                                                                                                                                                                                                           47.9%; Score 1115.5; DB 8; Length
50.3%; Pred. No. 9.3e-104;
.ive 71; Mismatches 138; Indels
6; 50pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS15771 standard; protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDF--HDVKEWTNVQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || | : ||::|
MDLPKSDAEGWTDIQ 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                        219; Conservative
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
õ
                                                                                                                                                                                                                                                    Sequence 444 AA;
SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                               68
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                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NYRYISTPEEFREYLP--ILKGPLPNWRGYVLDGDNGWLHARDSLKSAYEECK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|:: | || || :| || 342 YINLIVASGDSGNSFKIMPIIGKYVSKVVTKGDKGLDPED-KECWKWRPE----TW-DK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 VRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTMMSIPFEKTOIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHSLVLGCGASGRGFKYLPSIG----NLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                            Novel fructosylamine oxidase protein, useful for spectroscopic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine and fructosyl valine compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 PTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to fructosylamine oxidase protein (I; ADS1571) and its coding sequence (II; ADS1572) from Pichia sp. preferably Pichia sp. N1-1 strain. (I) is useful for spectroscopic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine compounds, and electrochemical analysis of analyzing fructosyl valine by spectroscopy, which involves degrading HDAIC, fructosyl valine by spectroscopy, which involves degrading HDAIC, fructosyl valine or fluctosylamine, respectively. (I) is also useful for carrying out electrochemical analysis of HDAIC, fructosamine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKV----ISSGQYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 RMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.9%; Score 836.5; DB 8; Length 427; 39.6%; Pred. No. 1.8e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1.8e-75;
84; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |:|| || ::::|| :|
RGOVRWGGRYRVADLNEIEEWVSVE
                                                           17-MAR-2003; 2003JP-00116348
17-MAR-2004; 2004WO-JP003587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 39.69
Matches 176; Conservative
                                                                                                                                                                                                                                                     WPI; 2004-709934/69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|:| :
------DPEIVSQW 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 QEKGVKYISGKTKGDVQELILDDITGECKGVVTADGTRHEADVVILAAGAWTPSLLDVKG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                        Ä.
                                                                                                                                                                                                                                                                                                                                                The present invention relates to a DNA sequence (I, ADE81173), which is associated with ML-236B synthesis. (I) is useful for improving ML-236B production in a HMG-COA reducing—enzyme-inhibitor ML-236B producing microbe. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVRPGEDPNLVELTRPEOFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAAREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRMGVKFVTGTPQGRVVTLIFEN--NDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGY-TNMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 QSADGTMMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARICWCADTANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA associated with synthesis of ML-236B, useful for improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                  28.4%; Score 661; DB 7; Length 432; 35.7%; Pred. No. 1.2e-57; ive 68; Mismatches 168; Indels !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWR----DTLGRFGGPNRVMDFHDVKEWTNVQYRDIS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236B production in ML-236B producing microbe
                                                                                                                                                                                                                                                                                                                          Example 8; SEQ ID NO 41; 142pp; Japanese.
                                                                                enzyme; Orf20
                                                                                                                                                                              15-OCT-2001; 2001JP-00316578
                                                                                                                                                                                                    15-OCT-2001; 2001JP-00316578
                                (first entry)
                                                                              ML-236B; HMG-CoA reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 35.7 es 163; Conservative
                                                                                                                                                                                                                            (SANY ) SANKYO CO LTD
                                                                                                      Penicillium citrinum
                                                                                                                                                                                                                                                    2003-817677/77.
                                                                                                                                                                                                                                                               N-PSDB; ADE81212
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 432 AA;
                                                                                                                              JP2003116567-A.
                               29-JAN-2004
                                                                                                                                                      22-APR-2003
                                                       Orf20, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
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          ADE81213;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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This sequence represents the fructosyl amino acid oxidase (FAOD-P) of the invention. This sequence was isolated from Penicillium janthinellum S-3413 (FERM BP-5475). FAOD-P oxidises amadori compounds in the presence of oxygen, producing alpha-ketoaldehyde, amine derivatives and hydrogen peroxide. FAOD-P is used in the detection of amadori compounds in, e.g. foods such as soy sauce, and in body fluids such as blood. This sequence, vectors containing it and host cells transformed by the vector are all used for the recombinant production of FAOD-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NNKDEIEVNEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GLEKTNIWLESEDDILAKAPH-FTREQIKGWKGLFCGDG-GWLAAAKAINAIGTFLKSQG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 NM-----VQSADGTWMSIPFEKTQ-----IPKEAETRVRALLKETWPQLADRPFSFARIC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 RNGPDLQ----LSLEALDMWKNDPLFKPFFHNVGMLDCSSSQEGIASLRRKHQDLDANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KSSSLLIV-GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 VKFGFGSAGTFKRPLFAPDGATCS-----GVETVDGTKYFADKVVLAAGAWSSTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 DFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Gaps
                                                                                                                                                                                                                                     compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fructosyl amino acid oxidase which oxidises amadori compounds DNA - used for detection of amadori compounds in foods and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.3%; Score 660; DB 2; Length 43 Best Local Similarity 33.6%; Pred. No. 1.6e-57; Matches 156; Conservative 75; Mismatches 157; Indels
                                                                                                                                                                                                                              Fructosyl amino acid oxidase; FAOD-P; enzyme; amadori alpha-ketoaldehyde amine derivative; amadori detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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AAW24134 standard; protein; 437
                                                                                                                                                                           Fructosyl amino acid oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-JP003651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95JP-00325672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOT-) KYOTO DAIICHI KAGAKU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tani Y,
                                                                                                                                                                                                                                                                                                                    Penicillium janthinellum
                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-332789/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-332789.
N-PSDB; AAT85703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                 WO9721818-A1
                                                                                                                16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1997
                                                          AAW24134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kato N,
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           287
                                                                                                                                                                                              61 NNKDEIEVNEILAERAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sent DNA sequence represents a fructosylamino acid oxidase (FAOD-
present sequence is derived from Penicillium janthinellum S-3413,
used to construct a synthetic sequence using primers AAX15951-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding fructosylamino acid oxidase - synthetically designed and
                                                                                                RFKLHQPYGATSPKLISVPRSHAKHPTDTYPDSSERTIRKALARFMPRFKDKELFNRSMC
                                                                                                                                                                335 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW
        DLEDQCVSKAWVFAHIQLTPQESAQYKDVPVVYDGDYGFFFEPN-EHGVIKVCDEFPGFS
                                                          285 NM-----VQSADGTMMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KSSSLLIV-GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fructosylamino acid oxidase; FAOD-P; Penicillium janthinellum S-3413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                         395 NP-----DIAANRNWRDTLGRFGGPNRVMDFHDVK 424
                                                                                                                                                                                                                                                                                                                           RPGGDALKSKRSAPAKDLAEMPGWK---------HDAK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.3%; Score 660; DB 2; Length 43 Best Local Similarity 33.6%; Pred. No. 1.6e-57; Matches 156; Conservative 75; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 10-12; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97387 standard; protein; 437 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A fructosylamino acid oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penicillium janthinellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinantly prepared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-208112/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX15950
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        229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a fructosylamino acid oxidase (PAOD-P), and is encoded by a synthetic sequence. The the wild type FAOD-P sequence is derived from Penicillium janthinellum S-3413. The synthetic sequence was constructed using primers AAX15951-6006
RFKLHQPYGATSPKLISVPRSHAKHPTDTYPDSSEETIRKAIARFMPRFKDKELFNRSMC 347
                                                    WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 394
                                                                                NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFKNQLRPTAWTLVHIALKPERRALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding fructosylamino acid oxidase - synthetically designed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pructosylamino acid oxidase; FAOD-P; Penicillium janthinellum S-3413.
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                                                                                                                                                        NP------DIAANRNWRDTLGRFGGPNRVMDFHDVK 424
                                                                                                                                                                                            28.3%; Score 660; DB 2; Length 437
33.6%; Pred. No. 1.6e-57;
ive 75; Mismatches 157; Indels
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                                                                                                                                                                                                                                                                                                                                            AAW97386 standard; protein; 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A fructosylamino acid oxidase.
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les 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Penicillium janthinellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinantly prepared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX15949
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The present sequence is the protein sequence of a novel fructosyl peptide oxidase (PPD) of Eupenicillium terrenum ATCC18547. FPO enzymes of the invention act on fructosyl valyl histidine in the presence of oxygen and catalyse a reaction that produces alpha-ketoaldehyde, valyl histidine and hydrogen peroxide. The E. terrenum FPO exhibits 182% relative activity for fructosyl gyroine and 9.78% for egsilon fructosyl lyapsine when compared to 100% activity for fructosyl valyl histidine. It shows optimal activity in the pH range 6.0-8.0 (preferably pH 7.0) and at temperatures around 35 degrees C, and is stable in the pH range 5.0-9.0 and at temperatures temperatures up to about 45 degrees C. The Km value for fructosyl valyl histidine is 4.25 mM. The E. terrenum cDNA can be used for mass
                                                                                                                                                                                                                                                                    284
                                   NM-----VQSADGTWMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARIC 334
                                                                                                                                                                                                    288 RFKLHQPYGATSPKLISVPRSHAKHPTDTYPDSSEETIRKAIARFMPRFKDKELFNRSMC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of the enzyme by recombinant methods. Stable FPO enzymes such as E. terrenum FPO are useful in clinical diagnosis, e.g. of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fructosyl peptide oxidases useful as enzymes for clinical diagnosis.
DFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT
                                                                                                                                                                                                                                                                                                                                                                                                            NP------DIAANRNWRDTLGRFGGPNRVMDFHDVK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 RPGGDALKSKRSAPAKDLAEMPGWK---------HDAK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fructosyl peptide oxidase; enzyme; diabetes; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eupenicillium terrenum fructosyl peptide oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kajiyama N;
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12-DEC-2001; 2001JP-00378151.
06-AUG-2002; 2002JP-00228727.
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Query Match 26.8%; Score 625; DB 6; Length 437; Best Local Similarity 34.2%; Pred. No. 5.7e-54; Matches 153; Conservative 81; Mismatches 174; Indels

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Title: Perfect score:

US-10-622-893A-1 63 1 MGGSGDDDDLAL 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

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Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Bukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzae, Oryza.
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Pred. No. 4.3;
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5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp[834223 Saccharomyces cerevisiae YBL058w SHP1
ORFNames=CAGL0A04345g;
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last e
Hypothetical protein P0495H05.26.
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69 LGGGGDDDSA 79
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnine=27.09107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnine=27. Eiglmeiner K., Camus J.-C., Medina N., Mansoor H.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

EMBL: BX248341; CAD956881.;

InterPro; IPR009515; DUF797.
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Sukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0085K21.17 (Hypothetical protein
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; APPOGS904; BAD26528.1; -.
EMBL; AP004863; BAD25559.1; -.
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SEQUENCE 64 AA; 6944 MW; 7D958B770D8766E3 CRC64;
                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Mb2135c.
OrderedLocusNames=Mb2135c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSJNBa0023117.33).
Name=OSJNBa0085K21.17; Synonyms=OSJNBa0023117.33;
                                                                                                                                                                                                                                                             64 AA
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Friedlin;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome I complete sequence.
ORFNAmes=CAGLO108305;
Candida glabrata CBS138.
Candida glabrata CBS138.
Sacharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TAXID=284593;
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MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2; Length 399;
Pred. No. 20;
                                                                                                          Score 46; DB 2; Length 392;
Pred. No. 20;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Friedlin;
Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL161416; CAB77684.1; -.
Hypothetical protein.
SEQUENCE 399 AA; 43458 MW; BB86021C2BBB3E18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                      392 AA; 43786 MW; 80FFF82FCB5E39EB CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein L4803.06.
                                                                                                                                                                                                                      399 AA
                                                                                                                100.0%; Prec. ...
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                InterPro; IPR006556; DUF FAFI.
InterPro; IPR009060; UBA_like.
InterPro; IPR001012; UBX.
Pfam; PF00708; UBX; 1.
SMART; SM00553; SEP; 1.
PROSITE; PSS0033; UBX; 1.
PROSITE; PSS0033; UBX; 1.
SEQUENCE 392 AA; 43786 MW; 81
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88.9%;
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         EMBL; CR380947; CAG57849.1;
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Best Local Similarity 88.9.
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Nature 430:35-44 (2004)
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
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Zeniou-Meyer M., Zivanovic I., Bolocin-Pukuhara M., Thierry A.,
Bouchler C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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Eukaryota, Euglenozoa, Kinetoplastida; Trypanosomatidae, Leishmania.
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M. Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (MUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL359773; CAB95222.1; -.
HSSP; Q92830; 1F68.
InterPro; IPR011487; Bromodomain.
InterPro; IPR011124; Znf_CW.
Pfam; PF07496; zf-CW; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CR380955; CAGG60546.1; -.

GO; GO:0008415; F:acyltransferase activity; IEA.

InterPro; IPR000542; Carn_acyl_trans.

Pfam; PF00755; Carn_acyleransf; 1.

SEQUENCE 951 AA; 106462 MW; PB5334D57409D4E1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mypothetical protein P1295.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1039 AA.
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Nature 430:35-44(2004).
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SEQUENCE FROM N.A.
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Q62134;
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Q6Z134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBb0086108.9 (Hypothetical protein OSJNBb0086108.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 45; DB 2; Length 586, 80.0%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jukanti A.K., Bruckner P.L., Fischer A.M.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AXS96266; AAT06523.1; -.
GO, GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Buell R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
[3]
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                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Polyphenol oxidase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008922; Di-copper centre.
InterPro; IPR00892; Hemocyanin.
InterPro; IPR00631; Tat.
InterPro; IPR005217; Tyrosinase.
Pfam; PF00264; Tyrosinase; 1.
PRINTS; PR00022; TYROSINASE.
IIGRAMS; TIGR01409; TAT signal seq; 1.
PROSITE; PS00210; HEMOCYANIN 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AA
                                                                                                                                                                                                          586 AA
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
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Matches 8; Conservative
                                                                                                                                                                                                      PRELIMINARY;
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                                      841 GGGGDDDDVPL 851
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36 GTGDDDDLVL 45
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                      Q6PLR1
Q6PLR1;
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SEQUENCE FROM N.A.
TOWN C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
Town C.D., Rooney T., Utterback T.R., Vanaken S.E., Feldblyum T.V.,
Tallon L.J., Rooney T., Utterback T.R., Vanaken S.E., Feldblyum T.V.,
White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 240;
                                                                                                                                                                                                                                                                                                                                                        2; Length 182;
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                                                                                                         SEQUENCE FROM N.A.

Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AC105746; AAM92808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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TOWN C.D., Kaul S.;
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, U93215; AAB63096.1; -.
PIR; H84708; H84708.
Hypothetical protein.
SEQUENCE 240 AA; 27400 MW; A6AB9BAF4EICFFCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                 Gramene, Q8L432; -.
Hypothetical protein.
SEQUENCE 182 AA; 19521 MW; BDD9842B26EB3F9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Pred. No. 25;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 AA.
                                                                                                                                                                                                                                                                                                                                                        69.8%; Score 44; DB 66.7%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=At2g30480;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JAN-2003 (TrEMBLrel. 24, Last ann
14-Ypothetical protein At2g30480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                EMBL; AC105746; AAM92811.1; -. EMBL; AE017066; AAP52498.1; -.
                                                                                                                                                                                                                                              EMBL; AE017066; AAP52503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.8%;
                                                                Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.7
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Best Local Similarity 77.0-
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1 MGGAGDDDRVEL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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163 VGGTGDDDD 171
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SEQUENCE FROM N.A.
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"Analysis and characterization of the complete genome of tupaia (tree shrew) herpesvirus.";
3. Virol. 75:4854-4870(2001).
EMBL; AP281817; AAK57076.1; -.
EMBL; AP281817; AAK57076.1; -.
Pfam; PF06070; Herpes UL32; 1.
PROSTIE; PS00583; PFKE KINAS. 1, UNKNOWN 1.
SEQUENCE 718 AA; 74589 MW; 92ED97DAC14EAS8F CRC64;
                                                                                                                                                                                                                                           PubMeda1244739; DOI=10.1038/nature01183; Feng O., Zhang Y., Huax., Jia P., Rang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Huax., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng O., Zhang L., Lu Y., Wu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tupaiid herpesvirus 1 (strain 1) (TuHV-1) (Herpesvirus tupaia (strain
                                                                                                 Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 AA; 72720 MW; DF79F807D9962BD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Herpesviridae,
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.8%; Score 44; DB 2; 80.0%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.8%; Score 44; DB 2;
88.9%; Pred. No. 89;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOI=10.1128/JVI.75.10.4854-4870.2001;
Bahr U., Darai G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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STRAIN=2;
MEDLINE=21211637; PubMed=11312357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420:316-320(2002).
EMBL; AL731606; CAE02429.1; -.
Gramene; QYXRMO; -.
SEQUENCE 652 Aa; 72720 MW;
  01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
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                                                             OSJNBa0058G03.4 protein.
Name=OSJNBa0058G03.4;
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Best Local Similarity
8, Conserve
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Best Local Similarity
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                    NCBI_TaxID=39947;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein At2g30480/T6B20.25.
Name=At2g30480/T6B20.25;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Call TaxID=3702;
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Xiao Y., Smith S.R., Ishmael N., Kumar N., Redman J., Riedmuller S., Utterback T., Whitelaw C.A., Fraser C.M., Town C.D.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY219097; AA037184.1; -.

Hypothetical protein.

SEQUENCE 621 AA; 71079 MW; A38A7DE170AFC9D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                            Oryza sativa (japonica cultivar-group).
Bukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0455F03.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005454; BAC84337.1; -.
InterPro; IPR00449; DUF266.
Pfam, PF03267; DUF266.
Pfam, PF03267; DUF266; 1.
SEQUENCE 359 AA; 39100 MW; C9FDD923301906CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22369114; PubMed=12481096; DOI=10.1104/pp.010207; Xiao Y.L., Malik M., Whitelaw C.A., Town C.D.; "Cloning and sequencing of cDNAs for hypothetical genes from chromosome 2 of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.8%; Score 44; DB 2; Length 621; 77.8%; Pred. No. 75; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2; Length 359;
Pred. No. 40;
2; Mismatches 2; Indels
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P0455F03.29.
Name=P0455F03.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 130:2118-2128(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    69.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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44 VGGGEDGDLAL 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGGSGDDDDLAL 12
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Best Local Similarity
8; Conserve
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                                                                                                                                                                 NCBI_TaxID=39947;
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Q84X11 Q84X11;

RESULT 13

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Query Match

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Q7XRM0 ID Q7XRM0 AC Q7XRM0; Q7XRM0;

RESULT 14

Search completed: May 27, 2005, 13:47:24 Job time : 6.63539 secs

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May 27, 2005, 13:47:36 ; Search time 126.721 Seconds (without alignments) 1189,648 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVTKSSSLLIVGAGTWGTST......MDFHDVKEWTNVQYRDISKL 437
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1: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

_	3, Appli 5, Appli	9, 7	8, Appli 3. Appli	1, 7	14478, A	 Appli 	68225, A	412, App	42701, A
Description	Sequence 3, Appli Sequence 5, Appli	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES ID	US-10-622-893A-3 US-10-622-893A-5	JS-10-470-678-9 JS-10-470-678-10	US-10-470-678-8 US-10-232-655-3	3-10-232-655-1	3-10-156-761-14478	3-10-829-427-1	JS-10-282-122A-68225	3-10-287-274-412	JS-10-282-122A-42701
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80	17	11	17	114	14	1,	끔	14	1;
% Query Match Length DB	437	4 4 4 4 0	440	139	384	387	385	433	433
% Query Match	100.0	49.4	49.4	25.8	7.9	7.1	7.1	6.9	6.9
Score	2329	1151.5	1149.5	600	184	166	165	160	160
Result No.	1 7	w 4	n o	. C 60	9	10	11	12	13

Sequence 9328, Ap	Sequence 55515, A				Sequence 75876, A		Sequence 72847, A		Sequence 177242,	Sequence 80, Appl	Sequence 69762, A	Sequence 14479, A	Sequence 30, Appl	Sequence 268694,		61710		11709	Sequence 27, Appl	Sequence 473, App	Seguence 10405, A	Sequence 56758, A	Sequence 8, Appli	Sequence 18, Appl	Sequence 2, Appli	Sequence 32, Appl	Sequence 68951, A	Seguence 9773, Ap	٠.	Seguence 168785,	Sequence 49792, A
14 US-10-156-761-9328	15 US-10-282-122A-55515	15 US-10-282-122A-43213		15 US-10-425-114-54552	15 US-10-282-122A-75876	9 US-09-815-242-13745	US-1	15 US-10-425-114-71622			15 US-10-282-122A-69762		9 US-09-873-880-30			15 US-10-282-122A-61710		16 US-10-437-963-117091	15 US-10-447-013-27	9 US-09-741-669-473	9 US-09-815-242-10405	15 US-10-282-122A-56758		15 US-10-415-302-18	US-1	9 US-09-873-880-32	15 US-10-282-122A-68951	15 US-10-369-493-9773			15 US-10-282-122A-49792
381	374	372	378	420	372	433	370	429	414	406	391	818	395	395	852	317	405	542	979	629	629	629	263	263	372	412	632	797	621	481	837
6.9	6.0	5.9	5.8	5.8	5.5	5.4	5.4	5.3	5.3	5.2	5.1	5.1	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.7
159.5	140	136.5	135.5	135	127	126.5	126	124	123	122	119.5	119.5	113.5	113.5	113.5	112.5	112.5	112.5	112.5	112.5	112.5	112.5	112	112	110.5	110.5	110.5	110.5	109.5	. 109	108.5
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A-3 No. US20050014935A1 No. US20050014935A1 ORNATION: Tuan, Chong-Sheng Datta; Abhijit Wang, Yuping NVERTION: METHODS AND COMPOSITIONS FOR ENCE: 466992001300 PLICATION NUMBER: US/10/622,893A LING DATE: 2003-07-17 SEQ ID NOS: 23 FastSEQ for Windows Version 4.0 Artificial Sequence A-3 100.0%; Score 2329; DB 17; Length 437; Similarity 100.0%; Score 2329; DB 17; Length 437; Similarity 100.0%; Pred. No. 3.7e-226; 7; Conservative 0; Mismatches 0; Indels 0; Gaps AVTKSSELLIVGAGTWGTSTALHLARRGYTNUTVLDPYPVPSALSAGNDVNKVISSGQYS NNKOBIEVNEILAEEAPNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL NNKOBIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL NNKOBIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL NNKOBIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGGVRVRPGEDPNL NNKOBIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGGVRYFYTG	RESULT 1 105-10-622-993A-3 105		,0 80)YS 60 YS 60	NL 120 NL 120	TG 180
Application US/10622893A No. US20050014935A1 No. US20050014935A1 Data; Chong-Sheng Data; Abhijit Wang, Yuping NUENTION: DETERMINATION OF GLYCATED PROTEINS ENCE: 46692001300 FILGATION NUMBER: US/10/622,893A LING DATE: 2003-07-17 SEQ ID NOS: 23 FESTSEQ for Windows Version 4.0 Artificial Sequence ORMATION: 40%-100% identity to the amadoriase A-3 100.0%; Score 2329; DB 17; Length Similarity 100.0%; Pred. No. 3.7e-226; 7; Conservative 0; Mismatches 0; Indels AVTKSSSLLIVGAGTWATSTALHLARRGYTNVTVLDPYPVPSALSAGND NNKDEIEVNEILAEERFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLG* NNKDEIEVNEILAEERFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLG* NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLG* NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLG* VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAARE	1-622-893A-3 1-622			VNKVISSG VNKVISSGQ	VRVRPGEDP VRVRPGEDP	aormgvkfv
Application US/10622893A No. US20050014935A1 No. US20050014935A1 ORWATION: Vara, Chong-Sheng Datta; Abhijit Wang, Yuping NETTION: WETHOON: WETHOODS AND COMPOSITIONS FOR NUMBER: US/10/622,893A LING DATE: 2003-07-17 ENCE: 466992001300 PLICATION NUMBER: US/10/622,893A LING DATE: 2003-07-17 SEQ ID NOS: 23 FastSEQ for Windows Version 4.0 Artificial Sequence ORWATION: 40%-100% identity to the amadori A-3 Artificial Sequence ORWATION: 40%-100% identity to the amadori A-3 AVTKSSSLLIVGAGTWGTSTALHLARRGYINVTVLDPYPVW NNKDEIEVNEILAEEAFNGWKNDPLFKPYTHDTGLLMSACS NNKDEIEVNEILAEEAFNGWKNDPLFKPYTHDTGLLMSACS VELTRPEOFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARN	1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A 1-622-893A-1 1-622-893A-1 1-622-893A-1 1-622-893A-3 1-622-8	INS	Length Indels	SAISAGND	QEGLDRLG QEGLDRLG	IALVAAARE
Application US/10622893A No. US20050014935A1 No. US20050014935A1 No. US20050014935A1 Datta; Abhijit Wang, Yuping WARTION: METHODS AND COMPOSITION NUENTION: DETERMINATION OF GLYCA ENCE: 466992001300 LING DATE: 2003-07-17 ENGERIE: 2003-07-17 FASTSEQ for Windows Version 4.0 37 Artificial Sequence ORMATION: 40%-100% identity to th A-3 INO. 0%; Score 2329; Similarity 100.0%; Score 2329; Similarity 100.0%; Pred. No. 3 AVTKSSSLLIVGAGTWGTSTALHIARRGYTNV NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHD	1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-62-893A-3 S FOR TED PROTE	, m	TVLDPYPVI TVLDPYPVI	TGLLMSACS	gagwaharn	
A-3 Application US/10622893A NO. US20050014935A1 NO. US20050014935A1 ORWATION: Vann, Chong-Sheng Datta, Abhijit Wang, Yuping NVENTION: METHODS AND COM NVENTION: DETERMINATION ENCE: 466922001300 LING DATE: 2003-07-17 SEQ ID NOS: 23 Artificial Sequence ORWATION: 40%-100% identi A-3 Artificial Sequence ORWATION: 40%-100% identi A-3 NVESSELLIVGAGTWGTSTALHI AVTKSSSLLIVGAGTWGTSTALHI NVEDIEVNEILAEEAFNGWKNDP NNKDEIEVNEILAEEAFNGWKNDP NNKDEIEVNEILAEEAFNGWKNDP NNKDEIEVNEILAEEAFNGWKNDP NNKDEIEVNEILAEEAFNGWKNDP	1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-893A-3 1-622-100 NO. US20050014935A1 1-62ATT: Van, Chong-Sheng PELICANT: Datta; Abhijit PELICANT: Datta; Abhijit PELICANT: Datta; Abhijit PELICANT: Wang, Yuping TLE OF INVENTION: METHODS AND COM TILE OF INVENTION: DETERMINATION THE OF INVENTION: DETERMINATION THE OF INVENTION: DETERMINATION THE REBERENCE: 46692001300 TRRENT APPLICATION NUMBER: US/10/6 RRENT APPLICATION NUMBER: US/10/6 RRENT APPLICATION NUMBER: US/10/6 RRENT APPLICATION NUMBER: US/10/6 FRENT APPLICATION: 40%-00.0%; SCO. TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: PRT TYPE: TOO NOS: 23 TYPE: TO	POSITION OF GLYCA 22,893A on 4.0	re 2329; d. No. 3 lismatche	ARRGYTNV ARRGYTNV	 	WKGYFARS
A-3 Application US/1 No. US2005001493 ORMATION: Yuan, Chong-Sher Datta; Abhijit Wang, Yuping WYENTION: METHODS WYENTION: DETERN FORE: 466920013R FUING DATE: 2003-23 FASTSEQ for Windc Artificial Seque ORMATION: 40%-100 Similarity 100. Similarity 100. A-3 WYENSSILIVGAGTW NYKDEIEVNEILAEEP NYKOSILIVGAGTW NYKOBIEVNEILAEEP NYKOSILIVGAGTW NYKOBIEVNEILAEEP NYKOBIEVNEILAEEP	P-622-893A-3 Puence 3. Application US/1 PERAL INFORMATION: PELICANT: Yuan, Chong-Sher PELICANT: Yuan, Chong-Sher PELICANT: Yuan, Chong-Sher PELICANT: Wang, Yuping TILE OF INVENTION: METHODE TILE OF INVENTION: METHODE TRENT PELLING DATE: 2003-MREEN OF SEQ ID NOS: 23 PERRENT FILING DATE: 2003-MREEN OF SEQ ID NOS: 23 PERRENT FILING DATE: 2003-MREEN OF SEQ ID NOS: 23 PERGANIEN: PERGANIEN: Artificial Seque TREATHE: TYPE: PRT TYPE: PRT TYPE: PRT TYPE: NYENCHMATION: 40%-10C -622-893A-3 I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I AVTKSSSLLIVGAGTW I I I AVTKSSSLLIVGAGTW I I I I I I I I I I I I I I I I I I I	.0622893A isAll isAND COM inATION 00 uS/10/6 .07-17 www Versi		GTSTALHI GTSTALHI	FNGWKNDP FNGWKNDP	sviqgdfpg
A-3 Applicat No. US20 ORMATION Yuan, Ct Dattai, Wang, WADEL WANTION NVENTION ENCE 466 PLICATION FASTSEQ JA Artifica ORMATION A-3 Artifica Artifica NVENTENE AVIKSSSI NVEDEIN NVEDEIN NVEDEIN NVEDEIN NVEDEIN NVEDEIN NVEDEIN	1-622-893A-3 1-622-893A-3 1-622-893A-3 1-6210ANT: YUAN, CI PELICANT: WANG, 'PLICANT: WANG, 'PLICANT: WANG, 'PLICANT: WANG, 'PLICANT: WANG, 'PLICANT: WANG, 'PLICANT: WANG, 'PLICANTION' THE OF INVENTION' THE OF INVENTION OF THE OF INVENTION OF THE OF INVENTION OF THE	tion US/1 005001493 cong-sher nong-sher nong-sher tuping merHODS merHODS S99200130 NUMBER: 3 2003-9 S9: 23 for Windc	vat	LIVGAGTW	NEILAEEP NEILAEEP	PRKLAPE C
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64 SKGDDEDSIWKALSYAAAQGWLHDPVFQPFCHNTGSVVAGSTPKSIKQL-VEDEIGDDID 122
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                                            ASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDF
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Publication No. US20050101771A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITION POR ASSAYING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P

CURRENT APPLICATION NUMBER: US/10/470,678

CURRENT PILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: UP 2001/ 22953

PRIOR PLING DATE: 2001-01-13

PRIOR PLING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

SEROR FILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.2

LUMBER 440
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ORGANISM: Artificial Sequence
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Best Local Similarity 51.0°
Matches 222; Conservative
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US-10-470-678-9
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                                                               TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI
                                                                                       181 TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI
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Publication No. US20050014935A1

GENERAL INFORMATION:

APPLICANT: Van, Chong-Sheng

APPLICANT: Ward, Abhijit

APPLICANT: Ward, Nuping

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS

FILE REFERENCE: 466992001300

CURRENT APPLICATION NUMBER: US/10/622,893A

CURRENT FILING DATE: 203-07-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: chimeric protein
US-10-622-893A-5
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Publication No. US20050101771A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   ## APPLICANT: KOUZUMA, Takuji et al.

TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
FILLE REFERENCE: 1516-0121P
CURRENT APPLICATION NUMBER: US/10/470,678
CURRENT PILING DATE: 2003-07-30
PRIOR PAPLICATION NUMBER: UP 2001/22953
PRIOR PILING DATE: 2001-013
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VETSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 1150.5; DB 17; Length 440; 51.0%; Pred. No. 5.3e-107;
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic protein sequence of SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Mismatches 131; Indels
                                                                US-10-470-678-10

'Sequence 10, Application US/10470678
; Publication No. US20050101771A1
; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDF--HDVKEWTNVQ 430
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                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
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TGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV 238
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GENERAL INFORMATION:

APPLICANT: KOUZUMA, Takuji et al.

TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: UP 2001/ 22953
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: UP 2001/ 24002
PRIOR APPLICATION NUMBER: UP 2001/ 24002
PRIOR SPEING DATE: 2001-02-16
PRIOR SPEING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 1149.5; DB 17; Length 440; 51.0%; Pred. No. 6.6e-107; tive 75; Mismatches 131; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic protein sequence of SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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MDLPKSDVEGWTNIK 437
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Best Local Similarity 51.04
Matches 222; Conservative
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APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAMA, NAOKI
TITLE OF INVENTION: NO. US2V
FILE REFERENCE: 227590USO
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; Sequence 8, Application US/10470678

RESULT 5 US-10-470-678-8

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SEQ ID NO'1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 ----GEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 QRMGVKFVTGTPQGRVVTLIF--ENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHFGYTNM-- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 QCVSKAWVFAHIQLTPKEADAYKAVPVVYDGEYGFFFEPN-EYGVIKVCDEFPGFSRFKL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 ---VQSADGTWMSIPPEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWÇAD 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 GQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRP-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                2 AHSRASIKVVVVGGGGIIGSSTALHLIRSGYIPSNITVLDVYKIPSLQSAGHDLNKIM-- 59
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APPLICANT: HINOKAWA, KOZO
APPLICANT: HINOKAWA, NOZO
APPLICANT: HINOKAWA, NOZO
TITLE OF INVENTION: NO. US20030157593Ale1 fructosyl peptide oxidase
FILE REFERENCE: 227590USO
CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: JP 2001-266665
PRIOR APPLICATION NUMBER: JP 2001-378151
PRIOR APPLICATION NUMBER: JP 2001-378151
PRIOR APPLICATION NUMBER: JP 2002-228727
PRIOR PILING DATE: 2003-13-12
PRIOR PILING DATE: 2003-13-13
PRIOR PILING DATE: 2003-28-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                          1 AVTKSSSLLIV--GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISS
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                                                                                                                                                                                                                                                                                                                  Length 437;
                                                                                                                                                                                                                                                                                                            26.8%; Score 625; DB 14; Length 43 34.2%; Pred. No. 7e-54; Artive 81; Mismatches 174; Indels
CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: UP 2001-266665
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: UP 2001-378151
PRIOR APPLICATION NUMBER: UP 2002-228727
PRIOR PILING DATE: 2001-12-12
PRIOR PILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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Publication No. US20030157593A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                       ORGANISM: Eupenicillium terrenum
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34.2'
Matches 153; Conservative
                                                                                                                                                                                                                 LENGTH: 437
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Sequence 5366, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovit, Vihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: UNCleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Uncleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 53616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 QIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGAS 362
                                                                                                                                                                                                                                                                                                                                                                   R---PEQFRKLAPEGVLQGD-FPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TPQGRVVTLIFENNDVK--GAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 HIQLTPEBAAEYKGVPVVYNGEFGFFFEN-EFGVIKVCDEFPGFSRFKEHQPYGAPSPK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 IEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL-VELT 124
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                                                                                                                                                                                                                                                                HIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQ-----SADGT
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9.0%; Score 210.5; DB 16; Length 139;
Best Local Similarity 33.6%; Pred. No. 9.7e-13;
Matches 44; Conservative 21; Mismatches 39; Indels 27;
                                                                                                                                Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNP-
                                                                                                                             25.8%; Score 600; DB 14; Length 4 32.7%; Pred. No. 2.4e-51; ive 86; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: 13394327.pep
US-10-767-701-53616
                                                                                                                                                        Best Local Similarity Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 -- DIAANRNWR 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 PKDLADMPGWK 432
; LENGTH: 437; TYPE: PRT; ORGANISM: Conlochaeta sp. US-10-232-655-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-767-701-53616
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                                                                                                                                  Query Match
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APPLICANT: FORUTAMA, KEISUKE
APPLICANT: FORUTAMA, KEISUKE
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, GENES AND RECOMBINANT DNAS THEREOF,
TITLE OF INVENTION: AND METHODS FOR PREPARING THE SAME
FILE REFERENCE: 252202US0
CURRENT APPLICATION NUMBER: US/10/829,427
CURRENT FILING DATE: 2004-04-22
PRIOR APPLICATION NUMBER: UP 2003-121533
PRIOR APPLICATION NUMBER: UP 2003-396807
PRIOR PILING DATE: 2003-04-25
PRIOR PILING DATE: 2004-04-12
PRIOR PILING DATE: 2004-04-12
PRIOR FILING DATE: 2004-04-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 RLGVRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 EINTR-WPG-----ITVPENYNAI-------FEPNSGVLFSENCIRSY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 IKICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARI 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 KNQLRPTAWTLVHIALKP------EERALYKN---IPV-IFNIERGFFFEPDEERGE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 166; DB 17; Length 387; Best Local Similarity 21.4%; Pred. No. 1.5e-07; Matches 89; Conservative 68; Mismatches 173; Indels 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VNEILAEEAFNGWKNDPLFKPYYHDTGLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic Peptide US-10-829-427-1
                                                               Sequence 1, Application US/10829427
Publication No. US20050026265A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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                                           -------RQPRDDLGTBFQKKWSWPKQK 106
GRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLG-----RFGGPNRV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 PLFKPYYHDTGLLMSACS----QEGLDRLGVRVR-PGEDPNLVELTRPEQFRKLAPEGVL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIERG--PFFEPDEERGEIKICDEHPGYTNWVQSADGTWM-----SIPFEKT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LHFEEPMTRW 176
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22.1%; Pred. No. 2.2e-09;
tive 60; Mismatches 139; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -HSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVPQKI 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INDEA, HARUO
APPLICANT: INDEA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-242
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
                                                                                                                                                                                                                                                                                                                                              ; Sequence 14478, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                    | |:|::| || || || ||:
GHGYKFVPKIGERIVDVMK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptomyces avermitilis
US-10-156-761-14478
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OMURA, SATOSHI
APPLICANT: ISEDA, HARUO
APPLICANT: ISHIKAWA, UIN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 22.1
Matches 101; Conservative
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|107 YHFDHI--WTN 115
                                                                                                                       MDFHDVKEWTN 428
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363
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Sequence 42701, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-282-122A-42701
                                            US-10-287-274-412
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                                                                              APPLICAMY: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 PGEDPNLVELTRPEOFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREA--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 ERG--FFFEEPDEERGE--IKICDEHPGYTNMVQSA-DGTWMSIPFEKTQIPKEAETRVRA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 -GOYSNNKDEIEVNEILAEEAFNGWK--NDPLFKPYYHDTGLLMSACSQEGLDRLGVRVR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-----AKAG-GIAHOR--LTAAEVEARFS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 -----QRMGVKFVTGT------TG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 DGKIWRAERTFLCAGAS-AGQFL-DFKNQLRPTAWTLVHIALKPEERALYKNIPV-IFNI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KSYTAVVVGLGVVGSATLWRLAQQ---QQDVL------GLEAGAPINLQGSSYGGSRIF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 ROAYWEGSDYLS----LLAEADLGWRELQATSHRPLLHYSG-------GLFIG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISS-----
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.8e-07;
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US-10-282-122A-68225
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23... Matches 101; Conservative
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Best Local Similarity
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Sequence 412, Application US/10287274

Sequence 412, Application US/10287274

Sequence 412, Application US/10287274

Sequence 412, Application US/10287274

Sequence 412, Application US. US2030181408A1

GENERAL INFORMATION:

APPLICANT: POLIGEN, Kari

APPLICANT: Zyskind, Judith

TILLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO

FILE REFERENCE: ELITRA.008DV1

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/164415

PRIOR PLING DATE: 1999-11-09

PRIOR PLING DATE: 1999-11-09

PRIOR APPLICATION NUMBER: US 09/711164

PRIOR PLING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 LSLGIVCPLSSLTQSRVPASELLTRFKAHPAVRPLIKNTESLEYGAHLVPEGGLHSMPVQ 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 -PGATVDALYEENGRVCGVICGD-DILRARYVVLAEGA------NSVLAERHGLV-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 VNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL---GVRVRPGEDPNLVELT 124
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6.9%; Score 160; DB 14;
Best Local Similarity 23.3%; Pred. No. 7.1e-07;
Matches 106; Conservative 49; Mismatches 146;
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; ORGANISM: Escherichia coli
US-10-287-274-412
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66 IEVN-EILAEEAFNGWKNDPLFKPYYHDTG--LLMSACSQEGLDRLGVRVRP--GEDPNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 F----VTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERIFLCA-----GASAGQF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 VLRHCEVTG-----IETRGDDITAVLTRRGRI--GTGTVICAAGAWSKAVGAMVGVD 217
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6.8%; Score 159.5; DB 14;
Best Local Similarity 23.3%; Pred. No. 6.5e-07;
Matches 96; Conservative 53; Mismatches 172;
337 ISACQHREPQNLFPL--YHHNVERSLLW-DVLQRY 368
                                                                                                                                                                                                                                                                                                        APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BAIRKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                   Sequence 9328, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Streptomyces avermitilis US-10-156-761-9328
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US-10-282-122A-55515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - PGATVDALYEENGRVCGVICGD-DILRARYVVLAEGA-----NSVLAERHGLV-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ALKPEERALYKNIPVIFN----IERGFFFEPDEERGEI---KICDEHPG----YTNMVQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 -TRPAGEAMALGIKEVLSLETSAIEBRFHLENNEGAALLFSGRICDDLPGGAFLYTNQOT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SADG-----TWMSIPFEKTQIPKEAETRVRALLKET------MPQ--LADRPFS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 LSLGIVCPLSSLTQSRVPASELLTRFKAHPAVRPLIKNTESLEYGAHLVPEGGLHSMPVQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FARICW-----CADTANREFLIDRHPQYHSLVLGCGASGRGFKY----LPSIGNLI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL---GVRVRPGEDPNLVELT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GISVRGMDMALTGAQAAAQTL 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 7.1e-07;
49; Mismatches 146; Indels 154;
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                                                                                                                                                                                                                                     TITLE REPERENCE: LOGATION OF ESSENTIAL CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: 00/191,078 PRIOR PLING DATE: 2003-02-20 PRIOR PELING DATE: 2000-03-21 PRIOR PLING DATE: 2000-05-23 PRIOR PLING DATE: 2000-05-24 PRIOR PLING DATE: 2000-05-26 PRIOR PLING DATE: 2000-05-26 PRIOR PRIOR DATE: 2000-05-26 PRIOR PRIOR DATE: 2000-05-26 PRIOR PRIOR DATE: 2000-05-26 PRIOR PRIOR DATE: 2000-05-09-06 PRIOR PRIOR DATE: 2000-09-09 PRIOR PLING DATE: 2000-09-09 PRIOR PLING DATE: 2000-09-09 PRIOR PLING DATE: 2000-09-09 PRIOR PLING DATE: 2000-10-23 PRIOR PRIOR DATE: 2000-110-23 PRIOR PLING DATE: 2000-110-27 PRIOR PLING DATE: 2000-11-27 PRIOR PLING DATE: 2000-11-27 PRIOR PLING DATE: 2000-11-27 PRIOR PLING DATE: 2000-12-22 PRIOR PLING DATE: 2000-12-22 PRIOR PLING DATE: 2000-12-22 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09 PRIOR PLING DATE: 2001-02-09
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                                                           Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Matches 106; Conservative
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APPLICANT: Travick, John
APPLICANT: Travick, John
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APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Yoreyth, R.
APPLICANT: Yu. H.
TILIE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034A
CURRENT PLILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PAPLICATION NUMBER: 60/206, 848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PELING DATE: 2000-12-22
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PRIOR PELING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 QFLDFKNQLRPTAWT---LVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICD 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 DRLGVRVRPGEDPNLVELTRPEQFRKL--APEGVLQGD--FPGWKGYFARSGAGWAHARN 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%; Score 140; DB 15; Length 374;
Best Local Similarity 20.7%; Pred. No. 5.9e-05;
Matches 90; Conservative 63; Mismatches 147; Indels 134; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Enterobacter cloacae US-10-282-122A-55515
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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ORGANISM:
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Oy 373 GNLIVDAMEGKVPQ 386

Db 348 GEIAAQFAGGIAPQ 361
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Search completed: May 27, 2005, 14:15:03 Job time : 128.721 secs

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GenCore version 5.1.6
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US-10-622-893A-3 2329 Title: Perfect score:

1 AVTKSSSLLIVGAGTWGTST........MDFHDVKEWTNVQYRDISKL 437 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

fructosyl amine -probable fructosyl sarcosine oxidase sarcosine oxidase L-pipecolate oxida dimethylglydine de probable D-amino a hypothetical prote sarcosine oxidase-probable sarcosine sarcosine oxidase, sarcosine oxidase, opine catabolism h probable oxidoredu thiamin biosynthes hypothetical prote hypothetical prote santhopine deamina hypothetical prote probable sarcosine probable sarcosine sarcosine oxidase fixC protein homol sarcosine oxidase sarcosine oxidase, sarcosine oxidase, probable dehydroge conserved hypothet Description SUMMARIES 140295 137605 150671 150671 150671 141246 144248 14424 144248 144248 144248 144248 144248 144248 144248 144248 14424 144248 14424 144248 14424 B % Query Match Length I 181 177.5 168 160 155 150 150 148 146 142.5 130.5 131 137.5 136.5 136.5 136.5 137.5 13 Score Result No.

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ALIGNMENTS

A P P P P P P P P P P P P P P P P P P P	RESULT 1 T40295 fructosyl amine - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03.05ec.1999 #sequence_revision 03-Dec.1999 #text_change 09.Jul-2004 C;Accession: T40295 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. A;Reference number: Z21918 A;Reference number: Z21918 A;Roteules: prollminary; translated from GB/EMBL,AL022071; PIDN:CAA17815.1; GSPDB:GN00067; SPDB:A;Roteiuental source: strain 972h-; cosmid c354 C;Genetics: A;Gene: SPDB:SPBC354.15 A;Map position: Z
OWE	Query Match 21.0%; Score 488.5; DB 2; Length 412; Best Local Similarity 30.1%; Pred. No. 5e-32; Matches 130; Conservative 78; Mismatches 183; Indels 41; Gaps 12;
ος Od	2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN 61 : :: : : : : : : 1 MVKNTSVIIVGAGVFGLSAALELTKRGGYTIKILDRAPPPVIDGSSVDANRIIRS-DYAD 59
δγ O	62 NKDEIEVNEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVR 113
P &	114 PGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRM 173
B &	174 GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIMRAERTFLCAGASAGQFL-DFKNQLRP 232
δγ DP	233 TAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDERGEIKICDEHPGYTNMVQSADG 292
ζζ Q	293 TWMSIPFEKTQIPKEAETRVRALLKETM-PQLADRPFSFARICWCADTANREFLID 347 : - - - - - - - - - -
& 43	348 RHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNW 404

405 RDTLGRFGGPNR 416

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C.Species: Streptomyces sp.
C.Jate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
C.Accession: JSo671, PSO345
B.Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
B.Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
B.Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
B.Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
B.Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
A.Reference number: JSO671; MUID:9233009; PMID:1368326
A.Reference number: JSO671; MUID:9233009; PMID:1368326
A.Residues: 1-389 <SUZ>
A.Residues: 1-389 <SUZ>
A.Suzuki, M.; Suzuki, M.
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A;Molecule type: protein
A;Residues: 2-31;122-143;230-259;268-283 <SUZ1>
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Comment: This enzyme catalyzes the oxidation of sarcosine to form formaldehyde, glycine
C;Superfamily: sarcosine oxidase
             A;Cross-references: UNIPROT:P40859; GB:D16521; NID:g984787; PIDN:BAA03967.1; PID:g984788 C;Genetics:
C;Genetics: Askidence: sox
C;Superfamily: sarcosine oxidase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 YYGFPSFGGCGLKLGYHTFGOKIDPDTINREFGVYPEDESNLRAFLEEYMPG-ANGELKR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 VNEILAEEAFNGWKNDPLFKPYYH----DTGLLMSACSQEGLDRLGVRVRPGEDPNLVEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TRPEQFRKLAPEGVLQGD-----FPGW---KGYFA--RSGAGWAHARNALVAAAREAQRM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EKTOIPKEAETRVRALLKETMPOLADRPFSF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 ARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVPQKI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 GAVCMYTKILDEHFIIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GPVHNRGSSHG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ----EALRSQELWYE--LEKETHHKIFTKTGVLV------FGPK---GESAFVAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 GAKVLTHT---RVEDFDISPDSVK-IETANGS-YTADKLIVSMGAWNSKLLSKLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGT
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                                                                                                                                                                                                                                                                                                                                                                              92;
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                                                                                                                                                                                                                                                                                       Length 390;
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F,2-389/Product: sarcosine oxidase #status experimental <SAR>
F,11-16/Region: nucleotide binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barcosine oxidase (EC 1.5.3.1) precursor - Streptomyces sp
                                                                                                                                                                                                                                                                                                                                                                              68; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.8%; Score 181; DB 2; Local Similarity 22.9%; Pred. No. 6.4e-07; les 100; Conservative 59; Mismatches 150.
                                                                                                                                                                                                                                                                                           8.2%; Score 192; DB 2;
23.2%; Pred. No. 8.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Conservative
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
A;Residues: 1-390 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 100
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule: type: DNA
A,Molecule: type: DNA
A,Residues: 1-433 <MCD>
A,Experimental source: strain 972h-; cosmid c139
A,Genetics SPB:SPAC139.04c
A,Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       astronine oxidase (EC 1.5.3.1) - Bacillus sp.

sarcosine oxidase (EC 1.5.3.1) - Bacillus sp.

c;Species Bacillus sp.

c;Species Bacillus sp.

c;Accession: 13975

s;Suzuki, K.; Sagai, H.; Imamura, S.; Sugiyama, M.

s;Suzuki, K.; Sagai, H.; Imamura, S.; Sugiyama, M.

A;Title: Cloning, sequencing, overexpression in Escherihia coil of a sarcosine oxidase-(A;Reference number: 139975

A;Reference number: 139975

A;Accession: 139975

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                                                                                                                                                                                                                                       probable fructosyl amino acid oxidase - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 C; Accession: T37605 R; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Saunders, D.; Harris, D. submitted to the EMBL Data Library, October 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 GOFLDFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEH 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAAAR 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSLLIVGAGTWGTSTALHLAR-RGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.0%; Score 465; DB 2; Length 433; 30.1%; Pred. No. 4.5e-30;
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        395 NPDIAANR-NWR 405
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	RESULT 6 T44248 sarcosine oxidase (EC 1.5.3.1) [imported] - Arthrobacter sp. (strain TE1826) C;Species: Arthrobacter sp. C;Species: Arthrobacter sp. A;Variety: strain TE1805 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 12-Jul-2004 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 12-Jul-2004 C;Accession: T4444 A;Reference number: 227,581-586, 1998 A;Reference number: 222735; MUID:99223334; PMID:9563845 A;Reference number: 222735; MUID:99223334; PMID:9563845 A;Reference number: 227735; MUID:99223334; PMID:9563845 A;Residues: 1-380 ANIS- A;Residues: 1-380 ANIS- A;Residues: 1-380 ANIS- A;Experimental Source: strain TE1826 C;Keywords: oxidoreductase	Query Match 7.2%; Score 168; DB 2; Length 389; Best Local Similarity 21.2%; Pred. No. 7.48-06; Matches 91, Conservative 68; Mismatches 171; Indels 100; Gaps 20; QY 13 AVTKSSLLIVGAGTWATSTALHLARRGYTNYTUDPYPPRAISAGNDVNKVISSGQYS 60 1: : : : : : : : :	RESULT 7 B65058 fixC protein homolog b2766 - Escherichia coli (strain K-12) N)contains probable quinone reductase (BC 1.6.5) C;Species: Escherichia coli C;Date: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 01-Mar-2002 C;Accession: B65058 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
OY 68 VNEILAEEAFNGWRXNDPLFKPYYHDTGLLMSACS-OEGLDRLGVRVRPGE 116		PESULT 5 JULY 6 JULY	OY 177 FVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWT 236 Db 175 VVBINP-GLLVTVKTTSRSYQAKSLVITAGPWTNQLLRPLGIE 216 QY 237 LVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPG 282 1

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A; Accession: E91081
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65058
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DNA
A;Residues: 1-433 < BLAT>
A;Cross-references: GB:AE000360; GB:U00096; NID:92367157; PIDN:AAC75808.1; PID:91789125;
C;Superfamilty: fixC protein
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                 125 RPEQFRKLAPEG----VLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                               97 ----FSSLOPGGESWSVLRARFDPW-------LVA---EAEKEGVECI-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 -PGATVDALYEENGRVCGVICGD-DILRARYVVLAEGA------NSVLAERHGLV-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ALKPEERALYKNIPVIFN----IERGFFFEPDEERGEI----KICDEHPG----YTNMVQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SADG-----TMMSIPFEKTQIPKEAETRVRALLKET------MPQ--LADRPFS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 FARICW-----CADTANREFLIDRHPQYHSLVLGCGASGRGFKY----LPSIGNLI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GISVRGMDMALTGAQAAAQTL 336
                                                                                                                                                                                                                                                                                                                                 68 VNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL---GVRVRPGEDPNLVELT 124
                                                                                                                                                                                                                                                                                                                                                                  96
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                                                                                                                                                                                                                                                                                       60 YTHALAE------LLPQFHLTAPLERRITHESLSLLTPDGVTT------
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   49; Mismatches 146; Indels 154;
                                                                                                                                                                                                 6.9%; Score 160; DB 1; Length 433; 23.3%; Pred, No. 3.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sarcosine oxidase (EC 1.5.3.1) - Bacillus sp
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                                                                                                                                                                                               6.9%
Query Match
Best Local Similarity 23.3%
Matches 106; Conservative
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Cipecies: Bacillus sp.
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Rivolama. Y. Yamamoto-Otake, H.; Suzuki, M.; Nakano, E.
Ajritle: Cloning and expression of the sarcosine oxidase gene from Bacillus sp. NS-129 in Ajritle: Cloning and expression of the sarcosine oxidates
Ajritle: Cloning and expression of the sarcosine to generate forms Bacillus sp. NS-129 in Ajritle: Cloning and expression of the sarcosine oxidase
Ajritle: Cloning and expression oxidase
Ajritle: Cloning and expression oxidase
Ajritle: Cloning and expression oxidase
Ajritle: Cloning and expression oxidase
Cj.Superfamily: sarcosine oxidase
Cj.Superfamily: sarcosine oxidase
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Best Local Similarity
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22;

78;

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LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE

94; Conservative

Matches

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A,Cross-references: UNIPROT:Q8X7T8; GB:BA000007; PIDN:BAB37044.1; PID:g13363092; GSPDB:GRA;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Escherichia coli (strain 0157:H7, substrain RIM
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H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 ---QFRKLAPEG----VLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LVA---EAEKEGVECI-- 130
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                                                                                                                                                          ELTRPEQFRKLAPEGVLOGDFPGWKG----YFA--RSGAGWAHARNALVAAAREAQRM 173
                                                                                                                                                                                                                                                                                                                                          --ERALYKN---IPV-IFNIERGFFFE-PDEERGEIKIC 277
                                                                 VNEILABEAFNGWKNDPLFKPYYHDTGLLM-----SACSOEGLDRLGVRVRPGEDPNLV 121
                                                                                                                                                                                                    113 SLEH-ELF-----EGKQLTD--RWAGVEVPDNYEAIFEPNSGVLFSENCIQAYRELAEAH 164
                                                                                                                                                                                                                                                   GVKFVTGTP--QGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLR 231
                                                                                                                                                                                                                                                                                             GATVLTYTPVEDFEVTEDLVTIKTAKGSYT-----ANKLVVSMGAWNSKLLSKLD--- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                 DEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCA 337
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Species: Becherichia coli
Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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K;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama,
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 433;
                                                                                                  6.4%; Score 150; DB 2; 22.9%; Pred. No. 0.00026;
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C,Superfamily: fixC protein
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A;Molecule type: DNA
A;Residues: 1-433 <HAY>
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santhopine deaminating protein [imported] - Agrobacterium tumefaciens (strain C58, Dupon-
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
                                                                            C'Accession: AB3160

R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gllet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:QBUXUS; GB:AE008687; PIDN:AAL45696.1; PID:gl7743424; GSPDB:G;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                  ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB3160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid
C;Superfamily: Sarcosine oxidase
                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-380 < KUR>
                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary A, Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: UNIPROT:Q8X7T8; GB:AE005174; NID:g12517227; PIDN:AAG57874.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein ygcN [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 16-Feb-2001 #text_change 09-Jul-2004 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C; Accession: F85926 F; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A; Reference number: A85480; MUID:21074935; PMID:11206551 Coli 0157:H7.
                                  : | : | : | : | 237 LSLGIVCPLSSLTQSRVPASELLARFXTHPAVRPLIKNTESLEYGAHLVPEGGLHSMPVQ 296
                                                                                                    -- CADTANREFLIDRHPQYHSLVLGCGASGRGFKY----LPSIGNLI 376
                                                                                                                                                      -----GISVRGMDTALTGAQAAAQTL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALKPEERALYKNIPVIFN----IERGFFFEPDEERGEI---KICDEHPG----YINMVQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | : | : | 337 ISIGIVCPLSSLTQSRVPASELLARFKTHPAVRPLIKNTESLEYGAHLVPEGGLHSMPVQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLVELTRPE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---QFRKLAPEG----VLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 CATTFSSIQPGGESWSVLRARFDPW-----------LVA---EAEKEGVECI-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 -TRPAGEAMALGIKEVLSLETSAIEERFHLENNEGAALLFSGGICDDLPGGAFLYTNQOT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 SADG------TMMSIPFEKTQIPKEAETRVRALLKET-------MPQ--LADRPFS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 FARICW-----CADTANREFLIDRHPQYHSLVLGCGASGRGFKY----LPSIGNLI 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 YTHALAR-----SLLPOFHLTAPLERRITHESL------SLLTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154;
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22.9%; Pred. No. 0.00026;
tive 49; Mismatches 148; Indels
  SADG------TWMSIPFEKTQIPKEAETRVRALLKET-
                                                                                                                                                                                                     377 VDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRF 411
                                                                                                                                                                                                                                     337 ISACQHREPQNLFPL--YHHЙVERSLLW-DVLQRY 368
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                                                                                                                                                      297 YAGNGWLLVGDALRSCVNT---
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Best Local Similarity 22.9
Matches 104; Conservative
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C,Superfamily: fixC protein
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Conserved hypothetical protein PA2776 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G3238
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Status: preliminary
A;Moldule type: DNA
A;Residules: 1-427 <STO>
A;Cross-references: UNIPROT:Q91067; GB:AE004705; GB:AE004091; NID:g9948851; PIDN:AAG0616
                                                                                                                                                                                                                                                                                                                                                                                                               66 IEVNEI----LAEE----AFNG---WKND----PLFKPYYHDTGLLMSACSOEGLD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 RLG----VRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 LVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQ 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 ICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICW 335
                                                                                                                                                                                                                                   12 SSAVIIGAGIFGVSTGVQLARRG-IQVTILNDGP-PANGASGRSLSWLNSARMRSEPYHQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 RLSAGDVARVTPGIDAGAI-----TPQGAI------FNPGEGWVDLPTL
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                                                                                                                                                                                 6 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
/ Match 6.4%; Score 148; DB 2; Length 380; Local Similarity 22.2%; Pred. No. 0.00031; nes 90; Conservative 51; Mismatches 151; Indels 114;
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
C;Accesion: B83078
S;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brandman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Olory, S.; Olson, M.V.
Jachy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Cross-references: UNIPROT:P33642; GB:AE004868; GB:AE004091; NID:g9950785; PIDN:AAG07934|
A;Experimental source: strain PAO1
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                                                                                                                                                                       295 QERDGLLFGPYESQEKMKLQASWVAHGVPPGFGKELPESDLDRI-----TEHVEAAMEM 348
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                                                                                                                                                                                                                                                                         349 VPVLKKADINIVNGPITYS----PDILP---MVGPHQGVRNYWVAIG-FGYGIIHAGG 399
                                                                                                                                                                                                                                                                                                                                                                                                     -----KWTTTQ 432
                                                          235 NRIVNAAGFWAREVGKMIGLDHPLIPVQHQYVVTSTIPEVKALKRELPVLRDLEGSYYLR 294
                                                                                                                                                                                                                                        VRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPS 371
                                                                                                                                                                                                                                                                                                                                                  372 IGNLIVD-AMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDVKEWTNVQ 430
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                                                                                                                                ---RGFFFEPDEERGEIKICDE-----HPGYTNMVQSADGTMMSIPFEKTQIPKEAETR
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                      ERTFLCAG---ASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.0%; Score 139.5; DB 2; Best Local Similarity 24.6%; Pred. No. 0.0014; Matches 103; Conservative 44; Mismatches 165;
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C;Superfamily: Sarcosine oxidase
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Siel33

dimethylglycine dehydrogenase (EC 1.5.99.2) - rat

dimethylglycine dehydrogenase (EC 1.5.99.2) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: Siel313

R;Lang, H.; Polster, M.; Brandsch, R.

Bur. J. Biochem. 198, 793-799, 1991

A;Title: Rat liver dimethylglycine dehydrogenase. Flavinylation of the enzyme in hepatoc

A;Reference number: Siel33; MUD:91266966; PMID:1710985

A;Accession: Siel33

A;Molecule type: mRNA

A;Residues: 1-857 claN>

A;Residues: 1-857 claN>

A;Cross-references: UNIPROT:Q63342; EMBL:X55995; NID:g56688; PIDN:CAA39468.1; PID:g56689

C;Keywords: flavoprotein; oxidoreductase
                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V-RPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AREAQRMGV--KF---VTG------TPQGRVVTLIFENNDVKGAVTGDGKIWRA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGARKYGVILIKYPAPVTSLKPRPDGTWDVETPQGSV--------RA 234
                                                                                                                                                                                                                                                                                                                                                     66 IEVN-----EILAEEAFNGWKNDPLFKPYYHDTGL------LMSACSQEGLDRLGVR 111
                                                                                                                                                                                                                                                                                                                                                                                       112 VRPGE--DPNLVELTRPEOFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAARE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 KQLWERYGHNQLEIMDAKRIR----EVVATDNYIG--GMLDMSG-GHIHPLNLALGEAAA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GYTNWVQSADGTMMSI----PPEKTQIPKEAFTRVRALLKETMPQLADRPFSFARICWCA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 NYLLDYYRLSGDKRLİYGGGVIYGARDPADIEAIIRPKMLKTFPQLKDVKIDFA---W-- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 VIIGGGCVGVSLAYHLAKAGMRDVVLLE----KSELTAGSTWHAAGLTTYFHPGINLKKI 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN-------DVNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 ISSGQYSNNKDEIEVNEILAEEAFN--GWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVR
                                                                                                                                                                                                                                             6 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
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                                                                                                                                   Length 427;
                                                                                                                                                                                        Indels
                                                                                                                                ; Score 146.5; DB 2;
; Pred. No. 0.00049;
59; Mismatches 164;
                                                     A,Gene: PA2776
C,Superfamily: hypothetical protein HI0499
A, Experimental source: strain PAO1
                                                                                                                                   6.3%;
                                                                                                                             Query Match
Best Local Similarity 23.74
Matches 98; Conservative
                         Genetics:
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Bate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C;Accession: A83905
R;Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Puji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Recession: A83905
A;Status: preliminary
A;Residues: 1-376 &STO>
A;Cross-references: UNIPROT:Q9KB87; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB057
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2041
C;Superfamily: Sarcosine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 138; DB 2; Length 376;
Best Local Similarity 22.3%; Pred. No. 0.002;
Matches 90; Conservative 62; Mismatches 185; Indels 66; Gaps 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVNEILABEAFN---GWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPG----EDPNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASA---GQFLDFKNQ 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 ADGTWMSIP-FEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TPDGQPIIGY 321
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303 PGSPEGIPY-----IGPVPGFDGLWLNTGHYRNGLVLAPASCRLLADLMSGREP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 VPEWEGWYLATGHSRHGVLLSGWTGHLVAEELEGK--DQSHKL 362
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18183, A
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Copyright (c) 1993 - 2005 Compugen Ltd.
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27	97.5	4.2	338	œ	-60-669-175-20677	Sequence	2067	Ø
28	97.5	4.2	426	9	-10-990-328A-11712	Sequence	117	Æ
53	97.5	4.2	464	œ	-60-643-717-6325	Sequence	6325	Ap
30	97.5	4.2	493	9	-10-990-328A-11713	Seguence	11713,	4
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200	24.0	. 4	# C	0 1	-80-674-609-61 -11-076-463-10016	Sequence	10,	1 4
98	94.5	1.4	530		-11-079-045-10019	Sequence	1001	(A
36	94.5	4.1	590	7	-11-031-175-10939	Sequence	109	K
40	93	4.0	339	7	-11-122-943-2	Sequence	2,	11
41	92.5	4.0	1664	ø	-10-450-763-44587	Sequence	4458	Ø
42	91.5	3.9	239	9	-10-703-032-122312	Sequence	122312	_;
43	91.5	3.9	276	~	-11-092-052-1920	Sequence	1920, Ap	Ap
4.	91.5	9.0	412	9	-10-863-245A-6	Sequence		11
45	91.5	3.9	539	9	US-10-467-657-3870	Sequence	3870,	Αp
					ALIGNMENTS			
RESULT	-				,			
US-60-643-7 ; Sequence	US-60-643-717-1; Sequence 1355	-13558 558, Appl:	ication	'Sn	17-13558 13558, Application US/60643717			
; GENE	GENERAL INFORMATION:	MATION:	د د					
, ,	TITLE OF INVENTION: Genes	ENTION:		and	Uses for Plant Improvement			
, FIL	FILE REFERENCE: 38-21 (53629) A	CE: 38-	21 (5362	4 (6				
	CURRENT APPLICATION NUMBER: US/60/643, CURRENT FILING DATE: 2005-01-12	ICATION NG DATE	NUMBER 2005	 10 G	3/60/643,717 -12			
, NUMBER	BER OF SE	OF SEQ ID NOS:	S: 19247	7				
SEQ :	SEQ ID NO 135 LENGTH: 459	œ n						
, ,		ASPERGILLUS		P.	NIDULANS FGSC A4			
US-60-	-60-643-717-1	-13558						
Query	Query Match	,4,50	9.29	96.99	215; DB 8; Length	459;		
Matches	8	Conse	vat		smatches	s 220;	Gaps	10;
ò	3 T	TKSSSLLI	VGAGTWG	rsT/	VIVE	NDVNKVIS	SGQYSN	61
ДD	. 2	KSIPIAI	: : IGDGAFG	-21	:			57
ò	62 N	KDĘIEVN	BILAEEAI	FNG	NKDŖIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGFDPNLV	LGVR VR PGI	SDPNLV	121
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Query Match
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                                                                                                                           TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLOOO728
CURRENT PILING DATE: 2005-04-04
RICHARD FILING DATE: 1999-10-05
RICHARD FILING DATE: 1999-10-05
RICHARD APPLICATION NUMBER: 60/157,832
RICHARD APPLICATION NUMBER: 60/160,191
RICHARD APPLICATION NUMBER: 60/160,191
RICHARD APPLICATION NUMBER: 60/161,932
RICHARD APPLICATION NUMBER: 60/161,932
RICHARD APPLICATION NUMBER: 60/164,769
RICHARD APPLICATION NUMBER: 60/164,769
RICHARD APPLICATION NUMBER: 60/175,693
RICHARD APPLICATION NUMBER: 60/175,693
RICHARD APPLICATION NUMBER: 60/144,831
RICHARD APPLICATION NUMBER: 60/144,831
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RRICHARD OF SEO IN MAC. 43000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 DRLGVRVRPGEDPNLVELTRPEQFRK----LAPEGVLQG----DFPGWKGYFARSGAGWA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 NELGAR-----NELLGPEALRORFPWLSTEGVELGCHGIDKEGWFD-----PWA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 HARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENND---VKGAVTGDGKIWRAERTF- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 ----LLMGYKKKARALGANFANGSVVG----FEWNDSGGLSGAVVDAGDVLQRTVKFD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LCAGASAGQ---FLDFKNQLRPTAWTLVHIALKPEERALY-----KNIPVI---FN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 TCVLAAGAYSGÓVARLAGIGDKBAKBÁSLSVALPVEPRKRYVÝVVSTQGKNCPGLATPLT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 IE-RGFFFEDD------EERGEIKICDEHPGYTNMVQSADGTMMSIPFEKTQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 IPKEAETRVRALLKETMPQLADRPFSFARI----CWCA----DTANREFLIDRHPQYHSL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 SCGVLIIGGGGMGASSAFWLKSRALQLGRKLNVLVVER-----DAGYTSASTVLSVGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SSSLLIVGAGTWGTSTALHLARRGY-----TNVTVLDPYPVPSAISAG-NDVNKVISSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 1.8%; Score 181.5; DB 7; Length 440; al Similarity 24.1%; Pred. No. 1.4e-07; 108; Conservative 57; Mismatches 149; Indels 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 FIAAGFSGHGIQOTPAVGRAISELILDGK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 VLGCGASGRGFKYLPSIGNLIVD-AMEGK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                          Sequence 4818, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: DROSOPHILA
RESULT 2
US-11-097-143-4818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-097-143-4818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4818
LENGTH: 440
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Best Local 3
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APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO1495
CURRENT APPLICATION UNDERS: US/10/990,328A
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 13084
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DETECTION AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 H-----ADPEERDCPTARTDI---GDVQILSSFVRDHLPDLKPEP-AVIESCMYTNTPD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 NEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLVELTRPEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 FRKLAPEGVLOGDFP-----GWKGYFARSGAGWAHARNALVA---AARE---AQRMGVK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 LVHIALKPEERALYKNIPVIFNIERGF-------FFEPDEERGEIKICDEHPG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 YTNMVQSADGTMMSIPFEKTQIPKEAETRV-RALLKETMPQLADRPFSFARICWCADTAN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 YTRMMHECYQIWAQ-----LEHEAGTQLH--RQTGLLLLGMKENQELKTIQANLSRQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 VVEINP-GLLVT------VKTTSRSYQAKSLVITAGPWTNQL-----LRPLGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : : | : : | : : | : : | : : | 217 MPLQTLRINVCYWREMVPGSYGSQAFPCFLWLGLCPHHIYGLPTGEYPGLMKVSYHHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 FVTGTPQGRVVTL1FENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 REFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 177.5; DB 6;
21.7%; Pred. No. 2.6e-07;
tive 66; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 177.5; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC;
TITLE OF INVENTION: BUCKODING HUMAN ENZYME PR:
TITLE OF INVENTION: USES THEREOF;
FILE REPERENCE: CLOO1495
CURRENT APPLICATION NUMBER: US/10/990,328A;
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 55824
SOFTWARE: PASISEQ for Windows Version 4.0;
SEQ ID NO 13083
RESULT 3
US-10-990-328A-13084
Sequence 13084, Application US/10990328A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.7%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: SOGABE, Atoushi

APPLICANT: OKA, Masanori

TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS FOR PRODUCING THE SAME AND

TITLE OF INVENTION: REAGENT COMPOSITION USING THE SAME
FILE REFERENCE: 235670

CURRENT APPLICATION NUMBER: US/10/534,583

CURRENT FILING DATE: 2005-05-11

PRIOR APPLICATION NUMBER: DF2003-014423

PRIOR APPLICATION NUMBER: DF2003-014423

PRIOR APPLICATION NUMBER: DF2003-011-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2003-11-13

PRIOR FILING DATE: 2003-02-12

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 1

SEQ ID NO 1
                                                                                                                                                          262
                                                                                                                                                                                                                       333
   273
                                                                                                                                                                                                                                                       263 ---CGLKIGYHTYGQQIDPDTINREFGAYQ---EDESNLRDFLEKYMPE-ANGELKRGAV 315
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                                                                                                KNOLRPTAWTLVHIALKP------EERALYKN---IPV-IFNIERGFFFEPDEERGE
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 167; DB 6; Length 389; Best Local Similarity 21.2%; Pred. No. 2.2e-06; Matches 91; Conservative 68; Mismatches 171; Indels 100;
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TYPE: PRT
ORGANISM: Arthrobacter SP. TE1826
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GENERAL INFORMATION:
APPLICANT: KIKKOWAN, Keisuke
APPLICANT: KAJIYAMA, Naoki
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, MODIFIED SARCOSINE OXIDASE GENES,
TITLE OF INVENTION: AND METHODS FOR PREPARING THE MODIFIED SCARCOSINE OXIDASES
CURRENT APPLICANTON NUMBER: US/10/990,477
CURRENT PILLING DATE: 2004-11-18
                                                                                                                                                66 IVIGAGIQGCFTAYHLAKH-RKRILLLEQFFLPHSRGSSHGQSRIIRKAYLE-----DF 118
                                                                                                                                                                                                                                                          119 YTRMMHECYQIWAQ-----LEHEAGTQLH--RQTGLLLLGMXENQELKTIQANLSRQRV 170
                                                                                                                                                                                                                                                                                                                                       129 FRKLAPEGVLOGDFP-----GWKGYFARSGAGWAHARNALVA---AARE---AQRMGVK 176
                                                                                                                                                                                                                                                                                                                                                                                                 EHQCLSSEELKQRFPNIRLPRGEVGLLDNSG-GVIYAYKALRALQDAIRQLGGIVRDGEK 229
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                                                                                                                                                                                                                69 NEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLVELTRPEQ 128
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                                                                                             9 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIEV 68
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llarity 21.4%; Pred. No. 1.5e-06;
Conservative 69; Mismatches 172; Indels
21.7%; Pred. No. 3.1e-07;
ive 66; Mismatches 174; Indels
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PRIOR FILING DATE: 2003-11-18
PRIOR PLIING DATE: 2004-06-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
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                                Conservative
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tes 89; Conserva
Similarity
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US-10-990-477-6
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Best Local S:
Matches 89
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Matches 8
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Query Match
Best Local Similarity 20.9
Matches 98; Conservative
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422 ---FDLIELDPN---
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ORGANISM: Homo sapiens
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                                                                                                                                                              TYPE: PRT
ORGANISM: Homo
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LENGTH: 866
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                                                                                                                                                                                                                            APPLICANT: FURUKAWA, Keisuke
APPLICANT: FURUKAWA, Keisuke
APPLICANT: FUNDENTON: MODIFIED SARCOSINE OXIDASES,
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES
FILE REFERENCE: 261714US0
CURRENT APPLICATION NUMBER: US/10/990,477
CURRENT PILING DATE: 2004-11-18
PRIOR FILING DATE: 2003-11-18
PRIOR FILING DATE: 2003-11-18
PRIOR FILING DATE: 2004-66-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 RELAVAKGAKILITYT---RVEDFEVSQDQVK-IQTANGS-YTADKLIVSMGAMNSKILISK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 LN------LDIPLOPYRQVVGFFDSNEAKYSNDVDYPAFMVEVPKGIYYGFPSFGG- 262
305 MPG-ATGELKSGAVCMYTKTPDEHFVIDLHPQFSNVALAAGFSGHGFKFSSVVGETLSQL 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 RLGVRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 EINTR-WPG-----ITVPENYNAI-------FEPNSGVLFSENCIRSY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AREAQRAGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 KNOLRPTAWTLVHIALKP-----EERALYKN---IPV-IFNIERGFFFEPDEERGE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 IKICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 ---CGLKIGYHTYGQQIDPDTINREFGAYQ---EDESNLRDFLEKYMPE-ANGELKRGAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 CWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVPQKI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 165; DB 6; Length 387; Best Local Similarity 21.4%; Pred. No. 3.3e-06; Matches 89; Conservative 68; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13788, Application US/10990328A; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Synthetic Construct US-10-990-477-2
                                                                                                                                                                             Sequence 2, Application US/10990477
GENERAL INFORMATION:
APPLICANT: KIKKOMAN CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                       364 AVTCKTEHDI 373
                                                    379 AMEGKVPQKI
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US-10-990-328A-13788
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LENGTH: 387
                                                                                                                                             RESULT 7
US-10-990-477-2
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ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 PFSFARICWCADTANREFLIDRHPOYHSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVP 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 IGLEHPLIPVQHQYVVTSTIPEVKALKRELPVLRDLEGSYYLRQERDGLLFGPYESQEKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 V-RPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAG---ASAGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 AAGARKCGALLKYPAP----VISLKARSDGTWDVETPQGSM-RANRIVNAAGFWAREVGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 LDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIE------RGFFFEPDEERGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 KVQDSWVTNGVPPGFGKELFESDLDRIMEHI-----KAAMEMVPVLKKADIINVVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO1495
CURRENT PAPLICATION NUMBER: US/10/990,328A
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FRACESEQ FOR Windows Version 4.0
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20.9%; Pred. No. 0.0003;
cive 73; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%; Score 148.5; DB 6; Best Local Similarity 20.9%; Pred. No. 0.00025; Matches 98; Conservative 73; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PR
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLOO1495
; CURRENT PEDPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FASLSEQ for Windows Version 4.0
; SEQ ID NO 13788
; LENGTH: 774
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
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378 DAMEGK 383
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151 MTRIGWHATEQYLIEPEKIQEMFPLINMIKVLAGLY------NPGDGHIDPYSLTMAL 202
                                  112 V-RPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KICDE-----HPGYTNMV--QSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADR 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAG---ASAGQF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 LDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIE------RGFFFEPDEERGEI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVODSWVINGVPPGFGKELFESDLDRIMEHI------KAAMEMVPVLKKADIINVVNG 370
                                                                                                                                        54 ISSGQYSNNKDEIEVNEILAEEAFN--GWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Atomi, Haruyuki
TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
FILE REPRESENCE: 490051.401USPC
CURRENT APPLICATION NUMBER: US/10/526,324
CURRENT PILING DATE: 2005-02-28
PRIOR PILING DATE: 2003-08-29
PRIOR PILING DATE: 2002-08-30
PRIOR PILING DATE: 2002-08-30
PRIOR PILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 2167
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 QKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDVKEWTNVQYRD 433
LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Thermococcus kodakaraensis KOD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ن.
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NAME/KRY: misc_feature
LOCATION: (786544)..(786546)
OTHER INFORMATION: n is a or
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LOCATION: (414542)..(414542)
OTHER INFORMATION: n is a or
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LOCATION: (786907)...(786907)
OTHER INFORMATION: n is a or
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NAME/KEY: misc_feature
LOCATION: (786890)..(786890)
OTHER INFORMATION: n is a or
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NAME/KEY: misc_feature
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US-10-526-324-372
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64 IRMMKRSVELWKGLKEELGYDVEFTQSGYLFLIYSEEELEAFNNNVRLQNRFGVPSR--- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 VNEI-LAEEAFNGWKNDPLFKPYYHDTGLLMSACSOEGLD------RLGVRVRPGE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AREAORMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDF 226
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Best Local Similarity 21.6%; Pred. No. 0.00036;
Matches 92; Conservative 55; Mismatches 157; Indels 122; Gaps
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LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a or c or g or
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ION: (839139)..(839139)
INFORMATION: n is a or c or
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LOCATION: (1128505)..(1128506)
OTHER INFORMATION: n is a or c or
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LOCATION: (1561477)..(1561477)
OTHER INFORMATION: n is a or c
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LOCATION: (1128517)..(1128518)
OTHER INFORMATION: n is a or c
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LOCATION: (1128539)..(1128540)
OTHER INFORMATION: n is a or c
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LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a or c
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LOCATION: (1128499)..(1128499)
OTHER INFORMATION: n is a or c
                                                                                NAME/KEY: misc feature
LOCATION: (1128488)..(1128488)
OTHER INFORMATION: n is a or c
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LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a or c
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OTHER INFORMATION: n is a or
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                                                                          US-10-526-324-29

Sequence 29, Application US/10526324

GENERAL INFORMATION:

APPLICANT: Lananaka, Takayuki

APPLICANT: Atomi, Haruyuki

TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF

TITLE OF INVENTION: THE SAME

TITLE OF INVENTION: THE SAME

FILLE REPERENCE: 490051-401USPC

CURRENT APPLICATION NUMBER: PCT/182003/003597

PRIOR FILING DATE: 2005-02-28

PRIOR APPLICATION NUMBER: JC 1202-319011

PRIOR FILING DATE: 2003-08-30

PRIOR PILING DATE: 2003-08-30

NUMBER OF SEQ ID NOS: 2167

SOFTWARE: Patentin version 3.1

SEQ ID NO S. 2167

SEQ ID NO S. 2167
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NAME/KEY: misc_feature
LCCATION: (786890)..(786890)
OTHER INFORMATION: n is a or c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1128488)..(1128488)
OTHER INFORMATION: n is a or c or g
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ION: (786507)..(786907)
INFORMATION: n is a or c or g
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LOCATION: (839139)..(839139)
OTHER INFORMATION: n is a or c or g
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LOCATION: (1128539)..(1128540)
OTHER INFORMATION: n is a or c or g
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LOCATION: (1128517)..(1128518)
OTHER INFORMATION: n is a or c
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NAME/KEY: misc_feature
NCATLON: (414542)..(414542)
OTHER INFORMATION: n is a or c
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NAME/KEX: misc_feature
LOCATION: (786944) ..(786946)
OTHER INFORMATION: n is a or c
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LOCATION: (1128499)..(1128499)
OTHER INFORMATION: n is a or c
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LOCATION: (1128505)..(1128506)
OTHER INFORMATION: n is a or c
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LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a or c
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LOCATION: (1567477)..(1561477)
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360 DGKTDK 365
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APPLICANT: Zhang, Bei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLAN
FILE REFERENCE: 38-21 (53596)
CURRENT APPLICATION NUMBER: US/60/669,241
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60560842
PRIOR APPLICATION NUMBER: 60560842
PRIOR PILING DATE: 2004-04-09
PRIOR PILING DATE: 2004-04-09
PRIOR PILING DATE: 2004-06-11
PRIOR PILING DATE: 2004-06-11
PRIOR PILING DATE: 2004-06-11
PRIOR PLING DATE: 2004-06-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 WAKLINAMAGIRTKIPIEP-----YKHQAVI------TQPIKKGSVKPMVISFRYGH 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 TNMVQSADGTWM-SIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANR 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 EFLI------DRHP-----QYHSLVLGCGASGRGFKYLPSIGNLIVDAM-EGK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 RLGVRVRPGEDPNLVELTRPEQFRKLAP-EGVLQGDFPGWKGYFARSGAGWAHARNALVA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLD 225
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                                                                                                                                                                                                                                                                                                                                                                                      4 KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
                                                                                                                                                                                                                                                                                                                                                                                                                      8 EKSEITIIGGGIVGVTIAHELAKRG-EEVTVIE----KRFIGSGSTFRCGTGIRQQFNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 FKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIK--ICDEHPGY
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  Query Match 5.6%; Score 130.5; DB 6; Length 386; Best Local Similarity 21.0%; Pred. No. 0.0037; Matches 93; Conservative 65; Mismatches 164; Indels 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 T----DLPAW-----WYD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28797, Application US/60669241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Monsanto Technology LLC
APPLICANT: Baum, James A
APPLICANT: Glibertson, Larry A
APPLICANT: Kovalic, David K
APPLICANT: LaRosa, Thomas J
APPLICANT: LaRosa, Thomas J
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: No. Wei
                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a or c or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a or c or g
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APPLICANT:
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14 IVVIGAGVCGLAAAHELSRRGHDDVVVLEKGQPFGEQSAG----LARIFRIAHRRESLC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 TRPEQFRKLAPEGVLQ----GDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --NNKDEIEVNEILAEE-AFNGW-----KONDPLFKPYYHDTGLLMSACSQEGLDR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 VELAKRSIELMKGFARELGINVWLRQGGYIFLAKTAPVAQRLERNVSL------HNR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LGVRVRPGEDPNLVELTRPEQFRKLAP------EGVLQGDFPGWKGYFARS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FLCAGA---SAGQFLDFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VNEILABEAFNGWKNDPLFKPYYHDTGLLMSACSQEG----LDRLGVRVRPGEDPNLVEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof CURRENT APPLICATION UNMER: 92(11/031,175
CURRENT APPLICATION UNMER: 2005-01-08
                                                                                                                                                                                                                                                                                                                                                                            8 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 FGVPTR-----LITPDEARGIVPGLTMKDCLIASYNPEDGVI---FP-WPFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.9%; Score 115; DB 7; Length 505;
Best Local Similarity 21.9%; Pred. No. 0.13;
Matches 92; Conservative 54; Mismatches 148; Indels 126; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQF-----LDFKNQLRPT
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 RLAFAARGWQRWEAEFGVGRLLGSEGFIAAGAAADGVAQAMERAGA------
                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                            Length 389;
                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                 96;
                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                         5.0%; Score 115.5; DB 22.2%; Pred. No. 0.081; ative 41; Mismatches
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 5809
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1503
LENGTH: 389
TYPE: PRT
                                                                                                                                                                       ; ORGANISM: Mycobacterium paratuberculosis
PCT-1B03-06509-1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9986, Application US/11031175 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9986
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                       Best Local Similarity 22.28
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-031-175-9986
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                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Homolog annotation: Hit ID=XP_319829.1; Match level="QueryCoverag
OTHER INFORMATION: =97%, HitCoverage=96%, E-value=1e-136, Identity=45%"; Hit descrip
OTHER INFORMATION: ENSANGPO000015949 [Anopheles gambiae]
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_3881; Strand=+; Position=84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Regents of the University of Minnesota and The United States of America APPLICANT: Recretary of Agriculture
TITLE OF INVENTION: Mycobacterial Diagnostics
FILE REFERENCE: 09531/112W01
CURRENT APPLICATION NUMBER: PCT/IB03/06509
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 10/137,113
PRIOR PLILNG DATE: 2002-04-30
PRIOR PLILNG DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Pfam annotation: Pfam ID=DAO; Match level="Score=211.2, E-valu; OTHER INFORMATION: -60, Copies=1"; Pfam description=FAD dependent oxidoreductase US-60-669-241-28797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSG---QYSNNKDEIEVNEILAEEAFN----GWKN----DPLFKPYYHDTGLLMSACSQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 EGL----DRLGVRVRPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIPVIFNIERGFFFEPD-----EERGEIKICDEHPGYTNMVQSADGTWMSIPFEKTQIP 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 KEAETRVRALLKETMPQLADR--PFSFARI--CWCA----DTANREFLIDRHPQYHSLVL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKGAVTGDGKIWRAERTFLCAGASAGQ---FLDFKNQLRPTAWTLVHIALKPEERALY-K 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 RGTHILQDNYNLQTSLGAK---VELLSPEKLKEKFPFMNTDGVA-----LGCHGLENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLIVGAGTWGTSTALHLARRGYTNVTVL----DPYPVPSAISAGNDVNK-----VI
                                                                                                                                                                                                                                                                                       LOCATION: (519)..(519)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.3%; Score 124.5; DB 8; Length 530; Best Local Similarity 21.4%; Pred. No. 0.02; Matches 94; Conservative 64; Mismatches 167; Indels 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 VAGFSGHGIQOSPAVGRAMM 502
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PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60617261
PRIOR FILING DATE: 2004-10-11
NUMBER OF SEQ ID NOS: 50011
SEQ ID NO 28797
LENGTH: 530
                                                                                                                                                                                                 ORGANISM: Lygus hesperus
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (519)..(519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-1B03-06509-1503
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Search completed: May 27, 2005, 13:51:55 Job time : 53.2473 sec8
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OTHER INFORMATION: 2Fe-2S ferredoxins iron-sulfur binding region proteins.
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00197A, p-value=OTHER INFORMATION: 8.342e-14, raw score of 18.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: DOMAIN:
LOCATION: (18)..(113)
OTHER INFORMATION: ParB-like nuclease domain identified by PFam, accession name OTHER INFORMATION: ParB-like nuclease domain identified by PFam, accession name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 AASNVDSFLANRDESVYGKGSANTDSGIAVRRAPASATGKTQHHPGPVMMYVENMLDQAF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 RGDIACDTVVLAAGAWSPQVAKLADVKLPNEPHR----HEILSTEPLKPFLG-PLVSVLD 359
                                                 RGFFFEPDEERGEI -- KICD - EHPGYTNMVQSADGTWMSIPFEKTQIPKEAETRVRALLK 317
                                                                             360 SGLYFS-QSMRGEIVGGMGDAKEPAGLNM---GSTLRFV-----SRFAQALM 402
                                                                                                                                              318 ETMPQLADRPFSFARIC--W--CAD-TANREFLIDRHPQYHSLVLGCGASGRGFKYLPSI 372
                                                                                                                                                                              69 -NEILAEEAFNGWKUDPLFKPYYHDTGLLMSACSQEGLDRL-------- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||: | : || : : | | : : | | 182
123 MSEIVRELSQLGWDDNKIGKELGMDSDEVLRLKQINGLQELFADRQYSRAWTLKLAQRSA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GVRVR------PGEDPNLVELTRPEQF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 RKLAP--EGVLQGDFPGWKGYFAR----SGAG-----WAHARNALVAAAREAQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 KKLNPHEHPVLHSD-QGWQYRMRRYQNILKEHGCGVTPIMSMRRWL-AKNRPQADVR--- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 RMGVKFVTGTPQGRV-----VTLIFENNDVKGAVTGDGKIWR------AERTF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | | | : | | | - --VIYNVRTPQDVIFADEWRNYPVTLVAENNVTEGFIA--GRLTRELLAGVPDLASRTV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCAGASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGF---FFEPDEE 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.6%; Score 108; DB 6; Length 796;
Best Local Similarity 20.0%; Pred. No. 1;
Matches 87; Conservative 51; Mismatches 118; Indels 178; Gaps
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                Sequence 48529, Application US/10450763 GENERAL INFORMATION:
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MTCGPA--PYMDWVEQ----
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ORGANISM: Homo sapiens
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20, Appli 38, Appli 192, Appli 160, Appl 160, Appl 66, Appl 17, Appl 17, Appl 17, Appl 17, Appl 17, Appl 17, Appl 18, Appl

S US-10-653-517-25 S US-10-653-46A-25 US-10-865-978-A-25 US-10-865-978-A-25 US-10-865-978-A-25 US-10-865-978-A-25 US-10-865-978-B-30 US-10-808-386-86 US-10-624-909-160 US-10-624-909-160 US-10-624-909-160 US-10-624-909-124 US-10-624-909-124 US-10-624-909-124 US-10-624-909-124 US-10-624-909-124 US-10-624-909-124 US-10-624-909-124 US-10-624-909-138 US-10-624-909-138 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146 US-10-624-909-146

Sequence Seq

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Sequence 8, Sequence 5, 2

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US-10-622-893A-5
; Sequence 5, Application US/10622893A
; Publication No. US20050014935A1
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Sequence 9, App
Sequence 26, App
Sequence 8, App
Sequence 6, App
Sequence 6, App
Sequence 7, App
Sequence 25, App
Sequence 25, App
Sequence 25, App
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-467-243-8
US-10-270-223-4
US-10-239-652A-8
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US-10-622-893A-5
US-09-923-304-9
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Maximum Match 100%
Listing first 45 summaries
                                                               protein search, using sw model
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Match Length
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FEATURE:
OTHER INFORMATION: 40%-100% identity of the second bacterial leader sequence
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                                                                                                       Sequence 4 Application US/10622893A

Publication No. US20050014935A1

GENERAL INFORMATION:

APPLICANT: Vuan, Chong-Sheng

APPLICANT: Wang, Yuping

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS

TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS

TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS

CURRENT APPLICATION NUMBER: US/10/622,893A

CURRENT APPLICATION NUMBER: US/10/622,893A

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
ALIGNMENTS
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 17; Conservative
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PEATURE:
OTHER INFORMATION: 1gK Secretion Signal Sequence, Corin AA 787 to 796, Enterokinase
OTHER INFORMATION: Site, Corin AA 802 to 1042, and C-Terminal V5 and 6xHis Tags
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                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/10467243
; Sequence 26, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
APPLICANT: Haaning, Jeeper Mortensen
APPLICANT: Halkier, Torben
; TITLE CO INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
FILE REFERENCE: 0226w0310
; CURRENT FAPPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-03-03
; PRIOR FILING DATE: 2001-03-03
; PRIOR FILING DATE: 2001-03-03
; PRIOR FILING DATE: 2001-03-03
; PRIOR FILING DATE: 2001-03-03
; RUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
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; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Hanning, Jesper Mortensen
; APPLICANT: Hanning, Jesper Mortensen
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                       Query Match 65.0%; Score 58.5; DB Best Local Similarity 57.1%; Pred. No. 0.93; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   293 KGELGTELGSEGKPIPNPLLGLDSTRTG 320
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                                                                  TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                  US-10-865-978-37
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             SEQ ID NO 37
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Publication No. US20050003416A1

Publication No. US20050003416A1

APPLICANT: No. US20050003416A1

APPLICANT: Wu, Qingyu

TITLE OF INVENTION: Uses Thereof

FILE REPERENCE: 53103AUST1

CURRENT APPLICATION NUMBER: US/10/865,978

CURRENT APPLICATION NUMBER: US/10/865,978

CURRENT APPLICATION NUMBER: US/10/865,978

CURRENT APPLICATION NUMBER: US/10/865,978

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CORRENT APPLICATION NUMBER: US/10/865,978
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| Patent No. US2002001612A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: KATZ, RUTH
| APPLICANT: UTANG, FENG
| TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
| FILE REPERENCE: UTANG-056803
| CURRENT FILING DATE: 2001-08-06
| NUMBER OF SEQ ID NOS: 11
| SEQ ID NO 9
| SEQ ID NO 9
| LENGTH: 146
| TYPE: PRT
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100.0%; Score 90; DB 17; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Yuan, Chong-Sheng
APPLICANT: Datta, Abhijit
APPLICANT: Datta, Abhijit
APPLICANT: Batta, Abhijit
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
FILE REFERENCE: 4669292001300
CURRENT APPLICATION NUMBER: US,
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 472
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Matches 16; Conservative
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US-10-865-978-37
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US-09-923-304-9
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Sequence 4, Application US/10415232;
Sequence 4, Application US/10415232;
Publication No. US20040096435A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Metabolism;
TITLE OF INVENTION: Metabolism;
TITLE OF INVENTION: Metabolism;
FILE REFRENCE: 04511.0065. NPUSGO1;
CURRENT APPLICATION NUMBER: US/10/415,232
CURRENT FILING DATE: 2003-04-25;
PRIOR APPLICATION NUMBER: US C/243,009
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roberto Justo De Antueno; Stephen John Allen
TITLE OF INVENTION: Polymuclectides that Control Delta-6-Desaturase Genes
TITLE OF INVENTION: and Methods for Identifying Compounds for Modulating
FILE REFERENCE: 42320-0010
CURRENT APPLICATION NUMBER: US/10/239,652A
CURRENT PLING DATE: 2003-07-28
PRIOR PLING DATE: 2003-07-28
PRIOR PLING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEO ID NOS: 70
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Publication No. US20040053234A1
GENERAL INFORMATION:
APPLICANT: Michael David Winther; Heidi Lynn Smith; Andre Ponton;
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Pred. No. 1.4;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.0%; Score 58.5; DB 15; Best Local Similarity 59.1%; Pred. No. 1.4; Matches 13; Conservative 1; Mismatches 3;
                                                                                                        Score 58.5; DB 15;
Pred. No. 1.4;
                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                       446 RGPFEGKPIPNPLLGLDSTRTG 467
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                                                                                                        65.0%;
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                                                                                                          Query Match
Best Local Similarity 59.1'
Matches 13; Conservative
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Best Local Similarity
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ORGANISM: Human
       ; TYPE: PRT
; ORGANISM: rat
US-10-239-652A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pate
SEQ ID NO 8
LENGTH: 473
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| Publication No. US20030143634A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Bioimage A/S
| TITLE OF INVERTION: INTRACT LIVING CELLS, AND TO EXTRACT QUANTITATIVE INFORMA-TION REFINE REPERENCE: 9759-0126P
| TITLE OF INVERTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
| TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
| FILE REFERENCE: 3759-0126P
| CURRENT APPLICATION NUMBER: US/10/270,223
| CURRENT PILING DATE: 2002-10-11
| SOFTWARE: Patentin version 3.1
| SOFTWARE: Patentin version 3.1
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US-10-467-243-8
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                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
PRIOR APPLICATION NUMBER: DK PA 2001 00498
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/278,320
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PaetSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Aequoria Victoria and Human US-10-270-223-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 RGPFEGKPIPNPLLGLDSTRTG 343
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Best Local Similarity 59.1%;
Matches 13; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                            Sequence 25, Application US/09213888A

Sequence 25, Application US/09213888A

Sequence 25, Application US/09213888A

Sequence 25, Application US/09213888A

SEPLICANT: Gurney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Li, Jinhe E.

APPLICANT: Palarmacia & Upjohn Company

TITLE OF INVENTION: Haman Sel-10 Polypeptides and Polymucleotides that

TITLE OF INVENTION: Encode Them

FILE REPERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/213,888A

CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 25

LENGTH: 669
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APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REPERENCE: 6142
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 669
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OTHER INFORMATION: Description of Artificial Sequence: V5HIS tagged
OTHER INFORMATION: homo sapien
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US-09-328-877A-25
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65.0%; Score 58.5; DB 9;
Best Local Similarity 59.1%; Pred. No. 2.1;
Matches 13; Conservative 1; Mismatches 3;
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642 RGPFEGKPIPNPLLGLDSTRTG 663
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US-09-328-877A-25
Sequence 25, Application US/09328877A
Patent No. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
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ORGANISM: Artificial Sequence
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Best Local Similarity 59.1
Matches 13; Conservative
                                                                                       RESULT 11
US-09-213-888-25
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RESULT 13
US-10-653-497-25

Sequence 25, Application US/10653497

Publication No US20040110202A1

GENERAL INNORMATION:

APPLICANT: Li, Jinhe

APPLICANT: Li, Jinhe

TILLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

TILLE OF INVENTION: Encode Them

TILLE OF INVENTION: Bracke Them

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US-10-653-517-25
Sequence 25, Application US/10653517
Publication No. US20040115700A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: 05/068,243
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORWATION: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: homo sapien
US-10-653-517-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.0%; Score 58.5; DB 16; Best Local Similarity 59.1%; Pred. No. 2.1; Matches 13; Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KGELEGLPIPNPLL----RTG 17
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RESULT 15

US-10-653-496A-25

Sequence 25, Application US/10653496A

Publication No. US20040116672A1

GENERAL INFORMATION:

APPLICANT: Ourney, Mark E.

APPLICANT: Li, Jinhe

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

TITLE OF INVENTION: Encode Them

FILE REPRENCE: 6142

CURRENT APPLICATION NUMBER: US/10/653,496A

CURRENT FILING DATE: 2003-09-02

PRIOR PILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO S.5

LENGTH: 669

TYPE: PRT

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: V5HIS tagged
, OTHER INFORMATION: homo sapien
US-10-653-496A-25
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Search completed: May 27, 2005, 14:15:04 Job time : 5.92964 secs

1 KGELEGLPIPNPLL ----RTG 17

qq Š

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 27, 2005, 13:28:05 ; Search time 6.45203 Seconds (without alignments) 1019.048 Million cell updates/sec

US-10-622-893A-4 90

1 KGELEGLPIPNPLLRTG 17 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A Geneseq 16Dec04:* .. Database

geneseqp1990s:* geneseqp2008:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	αı	Description
1	59.5	66.1	32	8	ADN61411	Adn61411 Paenibaci
7	59	9.59	146	S	AAU76975	Aau76975 Human tra
е	58.5	65.0	42	œ	ADN40846	Adn40846 Synthetic
4	58.5	65.0	250	4	AAB20357	Aab20357 Anti-chel
'n	58.5	65.0	254	ω	ADQ98103	Adq98103 Chimeric
9	58.5	65.0	254	ω	ADQ98105	Adq98105 Chimeric
7	58.5	65.0	254	œ	ADQ98104	Adq98104 Chimeric
80	58.5	65.0	254	ω	ADQ98107	
σ	58.5	65.0	254	œ	ADQ98106	Adq98106 Chimeric
10	58.5	65.0	254	α,	ADQ98108	Adq98108 Chimeric
11	58.5	65.0	338	'n	ABG71834	Abg71834 Soluble h
12	58.5	65.0	349	ß	ABG71826	Abg71826 Protein e
13	58.5	65.0	368	9	ABR40351	Abr40351 Human ami
14	58.5	65.0	374	ო	AAB10639	Aab10639 Human VEG
15	58.5	65.0	473	4	AAE11082	Aae11082 C-termina
16	58.5	65.0	473	4	AAE11084	Aae11084 C-termina
17	58.5	65.0	473	S	AAE14740	Aae14740 C-termina
18	58.5	65.0	699	7	AAY22470	Aay22470 Human Cte
19	58.5	65.0	699	4	AAB59202	Aab59202 C-termina
20	56.5	62.8	253	œ	ADJ62976	Adj62976 Novel flu
21	Ġ.	62.8	361	ø	ABR61836	
22	9	62.8	383	Ŋ	ABB07412	Abb07412 Amino aci
23	56.5	62.8	383	9	ABG72053	Abg72053 Human HsK
24	55.5	61.7	570	80	ADR86696	Adr86696 Ephrin B4
25	55.5	61.7	570	œ	ADR82643	Adr82643 Human B4E

Human Human Viral	Viral Viral Viral Viral	Novel Novel Novel Novel	Adj63128 Novel flu Adj63012 Novel flu Adj63082 Novel flu Adj63058 Novel flu Adj63144 Novel flu Adj63022 Novel flu Adj63080 Novel flu
	ADQ48585 ADQ48573 ADQ48581 ADQ48577 ADQ48579	ADJ63148 ADJ63042 ADJ63116 ADJ63004 ADJ63024	8 ADJ63128 8 ADJ63012 8 ADJ63058 8 ADJ63058 8 ADJ63144 8 ADJ63022 8 ADJ63080
1620 8 1653 8 28 8	20000		233 233 233 233 233 233 233 8
61.7	57.25	57.2 57.2 57.2 57.2 57.2	57.2 57.2 57.2 57.2 57.2 57.2 57.2
	51.5 51.5 51.5 51.5	51.5 51.5 51.5 51.5	51.5 51.5 51.5 51.5 51.5 51.5
26 27 28	3370 A	3 3 3 4 4 2 6 6 8 7 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 1 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

ADN61411 standard; peptide; 32 AA. ADN61411; ADN6141]

01-JUL-2004 (first entry)

Paenibacillus sp. Cry1529-related V5 Ab epitope/His tag purity peptide.

Cry; toxic; lepidopteran pest; toxin complex; insecticide; DAS1529; ORF7; Cry1529; purification; V5 antibody epitope; H18 tag.

Synthetic. Unidentified

10. .26 /note= "V5 antibody epitope" Location/Qualifiers Key Region

WO2004002223-A2.

08-JAN-2004

27-JUN-2003; 2003WO-US020082.

28-JUN-2002; 2002US-0392633P. 21-JAN-2003; 2003US-0441647P.

(DOWC) DOW AGROSCIENCES LLC.

Merlo DJ; Zhu B, Bevan SA, Bintrim SB,

WPI; 2004-082821/08.

Screening a culture of Paenibacillus isolate for Cry protein or toxin complex protein, useful for controlling lepidopterans, comprises obtaining DNA or protein from the culture and assaying the presence of the gene or protein.

Example 11; Page 70; 220pp; English.

The invention relates to a novel method for screening a culture of a Paenibacillus isolate for a gene encoding a protein selected from a Cry protein that is toxic to a lepidopteran pest and a toxin complex protein. The method comprises obtaining DNA from the culture and assaying the DNA for the presence of the gene or obtaining a protein produced by the culture and assaying the presence of a protein that indicates the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying subject at risk for development of cancer, preferably lung cancer, comprises contacting RPL14, CD39L3, PMGM, or GC20 gene probe with test sample obtained from subject, and analyzing DNA from test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of identifying a subject at risk for the development of cancer, predicting progression or metastasis of non-small cell carcinoma and other carcinoma in a subject, or identifying an individual to be segregated from a high risk environment. The method comprises contacting an RPL14, CD313, PMGM, or GC20 gene probe with a test sample obtained from a subject, and analysing DNA from the test sample. The method is useful for identifying a subject (a smoker, non-
               Insecticide applications and may be useful for screening Paenibacillus sp. for toxin complex (TC)-like genes and proteins which may themselves be used to enhance or potentiate the activity of a stand-alone xenorhabdus toxin protein. The method may also be useful for screening Paenibacillus sp. and others for insecticidal thiaminase genes and proteins for controlling insects, particularly lepidopterans. The current sequence is that of the V5 antibody epitope/His tag purification peptide of the invention which was used to purify Paenibacillus sp. DAS1529 ORF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translation factor; suil; RPL14; CD39L3; PMGM; GC20; cancer; metastasis; carcinoma; non-small cell carcinoma; smoking; lung cancer;
                                                                                                                                                                                                                                                                                        Gaps
presence of the gene in the isolate. The method of the invention has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bladder cancer; head cancer; neck cancer; urothelial cancer; kidney cancer; bancers cancer; broat cancer; pharynx cancer; larynx cancer; larynx cancer; larynx cancer; upper airway primary cancer; upper airway primary cancer; upper airway primary cancer; upper airway secondary cancer; esophagus cancer; chromosome 3p21.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human translation factor suil homologue, GC20 in vector pCDNA3.1.
                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                 Score 59.5; DB 8; Length 32;
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                            ----RTG 17
                                                                                                                                                                                                                                                                                                                                                                 1 KGELNSKLEGKPIPNPLLGLDSTRTG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141. .146
/label= Histidine_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 78-79; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU76975 standard; protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001; 2001WO-US024718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-2000; 2000US-0222811P.
                                                                                                                                                                                                                                                     66.1%;
                                                                                                                                                                                                                                                                                                                                KGE----LEGLPIPNPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiang F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABK10353.
                                                                                                                                                                          Cry1529 protein.
                                                                                                                                                                                                             Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200212563-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002
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This invention relates to a novel method for producing a soluble RNA polymerase protein. Specifically, it refers to an RNA polymerase enzyme isolated from the post-transcriptional gene silencing (PTGS) pathway that is useful for in vitro RNA synthesis kits. The present invention describes an enzyme with enhanced solubility capable of producing two types of reaction products i.e. both short and long RNA copies. Purthermore, template including template length complementary RNA copies of the require a primer for initiation of RNA synthesis. As such, this method can also be used to produce radioactively or chemically labelled RNA probes for in situ hybridisation analyses or microarray work, to generate ringer RNA molecules to induce RNA interference effects in vivo and in vitro or to study nucleic acid secondary structure, nucleic acid-protein interactions. This
smoker or former smoker) at risk for the development, recurrence, or metastasis of cancer (preferably cancer of lung, bladder, head, neck, urothelial, kidney, pancreas, mouth, throat, pharynx, larrynx or esophagus, or an upper airway primary or secondary cancer), to identify subjects who need an intensive follow-up protocol and for the prognosis and diagnosis of cancer. This is the amino acid sequence of the human translation factor homologue suil/GC20 (located on chromosome 3p21.3, see AAU76974) and fragments of the vector pCDNA3.1/GS into which it is cloned in order to develop the gene probe described in the method of the
                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing nucleic acid product, involves contacting with template an RNA polymerase which produces short complementary RNA copies of template, that are scattered throughout entire template, and template-length
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic protein tag for an RNA dependent RNA polymerase SeqID 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase; post-transcriptional gene silencing; PTGS;
                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                       Score 59; DB 5; Length 146; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                       Query Match 65.6%; Score 59; DB Best Local Similarity 59.3%; Pred. No. 0.27 Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 114 KGELRGHPFEGKPIPNPLLGLDSTRTG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 15; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                            1 KGEL-----EGLPIPNPLL-----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray; RNA interference; tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN40846 standard; protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2003; 2003WO-FI000776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-2002; 2002US-0419562P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary RNA copies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bamford D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-399869/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RNAL-) RNA LINE OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADN40845
                                                                                                                                                                                                                                   Sequence 146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                               nvention
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(REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
polypeptide is an artificial tag protein sequence for an RNA polymerase of the invention.
                                                  Gaps
                                                                                                                                                                        Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour; cancer; therapy.
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                                                                                                                                                                                                                                                                                                                                  /label= CDR3
/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                     "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                "complementarity determining region 2"
                                  65.0%; Score 58.5; DB 8; Length 42; 59.1%; Pred. No. 0.086; ive 1; Mismatches 3; Indels
                                                                                                                                                          Anti-chelate antibody CHA255 Fab heavy chain.
                                                                                                                                                                                                               /label= FR1
/--re= "framework region 1"
                                                                                                                                                                                                                                                                          note= "framework region 2"
                                                                                                                                                                                                                                                                                                             /label= FR3
/note= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                              'note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                      245. .250
/label= Epitope_tag
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                AAB20357 standard; protein; 250 AA.
                                                              1 KGELEGLPIPNPLL----RTG 17
                                                                            15 RGPFEGKPIPNPLLGLDSTRTG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-1999; 99US-0156194P.
31-MAY-2000; 2000US-0208684P.
                                                                                                                                                                                                                                                                                 53. .68
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2000; 2000WO-US026619
                                                                                                                                                                                                                                      33. .37
/label= CDR1
                                                                                                                                                                                                                                                                   'label= FR2
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                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244971/25.
N-PSDB; AAF30632.
                     Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                           WO200122922-A2
                                                                                                                                                                                              Mus musculus
                                                                                                                                            11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2001
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                                                                                                                               AAB20357;
                                                                                                                                                                                                                                                                                                                                                                      Peptide
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Region
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The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The covalent bond. The present sequence is that of anti-indium-EDTA covalent bond. The present sequence is that of anti-indium-EDTA conduct-raided design was used to develop an indium-EDTA chelate to computer-aided design was used to develop an indium-EDTA chelate to computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently conducted the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a chuman/mouse chimeric Pab fragment that could be expressed in Bscherichia coll, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Pab can be conjugated to a targeting molety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Aban-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. Such engineering is typically accomplished by site-directed mutagenesis of a nucleic acid encoding the wild-type of the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine; mouse; chimeric; human; TTCH; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; V5 epitope; His tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%; Score 58.5; DB 4; Length 250; 59.1%; Pred. No. 0.57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.57
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 RGPFEGKPIPNPLLGLDSTRTG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RTG 17
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Example 4; Fig 15; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2003; 2003US-00350555.
22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KGELEGLPIPNPLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO2004065569-A2
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Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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/note= "Wild type Gly substituted for Cys"

Misc-difference 87

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This invention relates to multi-functional antibodies that recognise chelating agents and metal chelates, particularly macrocyclic metal chelate bend to an antigen recognition down to employ that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate bas a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cavalent bond between the reactive site of the antibody and the reactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody of comprises a targeting moiety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex. On addition of the metal chelate, a cell-antibody-metal chelate complex. Seconance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is a chimeric mutine antibody 2D12.5 variable heavy chain protein fused to the human anti-tetanus toxin antibody CHI heavy chain constant region
                                                                                                                                                       vel mutant antibody comprising reactive site not present in wild-type antibody and antigen recognition domain that recognizes macrocyclic al chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a V5 epitope and (His)6 tag, given in an exemplification of
                                                                                                                                                                                                                                                                                       Claim 41; SEQ ID NO 80; 208pp; English.
                           Corneillie T;
                                                                           WPI; 2004-580725/56
                                                                                                                                                                                                                                      autoimmune diseases
                                                                                                       N-PSDB; ADQ98096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 254 AA;
                           Meares C,
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65.0%; Score 58.5; DB 8; Length 254; 59.1%; Pred. No. 0.58; ive 1; Mismatches 3; Indels E
                                                                                                                     227 RGPFEGKPIPNPLLGLDSTRTG 248
                                                                               1 KGELEGLPIPNPLL----RTG 17
                                          13; Conservative
  Query Match
Best Local Similarity
Matches 13; Conserv
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AD098105 standard; protein; 254 AA (first entry) 21-OCT-2004 RESULT 6 THE KENNE WAY TO SEE THE SEE T

Chimeric 2dVH-TTCH protein with tag and an N87D/G53C mutations SeqID 83.

Gaps

murine; mouse; chimeric; human; TTCH; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cellate; cell-antibody-metal chelate complex; emission tomography; V5 epitope; tag; mutant; mutein. His

Homo sapiens Chimeric. Mus musculus Synthetic ...r Misc-difference 53

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This invention relates to multi-functional antibodies that recognise chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate chas a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a caturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the creative functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody comprises a targeting motety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-mutant antibody complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide is the cutant protein sequence comprising a chimeric murine antibody 2012.5 cratiable heavy chain protein fused to the human anti-tetanus toxin antibody continue and a V5 epitope with (His)6 tag, given in an exemplification companied on the continue and mutant region (2dVH-TTCH) with NB7D and G53C antibody chain protein fused to the human anti-tetanus dominance the continue companies and continue and a V5 epitope with (His)6 tag, given in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel mutant antibody comprising reactive site not present in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
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                                        /note= "Wild type Asn substituted for Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 41; SEQ ID NO 82; 208pp; English.
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
                                                                                                                                                                                 23-JAN-2004; 2004WO-US001808
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                                                                                                                                                                                                                                                                                                                                                                   Corneillie T;
                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases.
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                                                                                        WO2004065569-A2
                                                                                                                                    05-AUG-2004
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Treater bound to an antigen recognition domain, where the metal charact character bound to an antigen recognition domain, where the metal character reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the carctive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody comprises a targeting molety that blads specifically to a cell via a cell surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide is the mutant protein sequence comprising a chimeric murine antibody 2012.5 variable heavy chain protein fused to the human anti-tetamus toxin antibody CH1 heavy chain constant region (20MH-TTCH) with an N87D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                    magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; V5 epitope; His tag; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Asn substituted for Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 41; SEQ ID NO 81; 208pp; English.
                    mouse; chimeric; human; TTCH;
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2003; 2003US-00350555.
22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
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N-PSDB; ADQ98097.
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                                                                                                                                                                                                                                                                                                          Key
Misc-difference 87
                                                                                                                                                                                                                                                                                                                                                                                            WO2004065569-A2
                                                                                                                                                                                                                    Homo sapiens.
Chimeric.
                                                                                                                                                                                               Mus musculus
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chelating agent rather of martial control and control metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate has a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the reactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate is considered to make its forming a cell-mutant antibody complex is formed that can be detected using emission tomography, magnetic
Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                 This invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                             Claim 41; SEQ ID NO 84; 208pp; English.
                                                                                                                                                                   autoimmune diseases
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13; Conservative

Query Match Best Local Similarity Matches 13; Conserv

Sequence 254 AA;

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Chimeric 2dVH-TTCH protein with tag and an N87D/G55C mutations SeqID 85.
                                                                                                                                                              magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; V5 epitope;
                                                                                                                                                                                                                                                                                                             note= "Wild type Gly substituted for Cys"
                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Asn substituted for Asp"
                                                                                                                                                      mouse; chimeric; human; TTCH; tetanus
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                  227 RGPFEGKPIPNPLLGLDSTRTG 248
17
                                                                      ADQ98107 standard; protein; 254 AA
1 KGELEGLPIPNPLL----RTG
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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                                                                                                              (first entry)
                                                                                                                                                                                                                   His tag; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-580725/56.
                                                                                                                                                                                                                                                                                                                         Misc-difference 87
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                                                                                                              21-OCT-2004
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                                                                                                                                                                                                                                                                       Synthetic
                                                                                          ADQ98107;
                                                                                                                                                                                                                                                           Chimeric.
                                                                                                                                                       murine;
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photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide is the mutant protein sequence comprising a chimeric murine antibody 2D12.5 variable heavy chain protein fused to the human anti-tetamus toxin antibody CHI heavy chain constant region (2dVH-TTCH) with NB7D and GS5C mutations and a VS epitope with (His)6 tag, given in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric 2dVH-TTCH protein with tag and an N87D/G54C mutations SeqID 84.
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 resonance imaging, lanthanide luminescence, gamma-emissions or single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; V5 epitope; His tag; mutant; mutein.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                  2,
                                                                                                                                                                                 Score 58.5; DB 8; Length 254;
Pred. No. 0.58;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Asn substituted for Asp"
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                                                                                                                                                                                                                                                                  1 KGELEGLPIPNPLL-----RTG 17
                                                                                                                                                                                                                                                                                                                                                      ADQ98106 standard; protein; 254 AA.
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59.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2003; 2003US-00350555
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corneillie T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-580725/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                          of the invention.
                                                                                                                                                      Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADQ98099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004065569-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                      ADQ98106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                        RESULT 9
8888888888888888
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Claim 41; SEQ ID NO 83; 208pp; English.

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This invention relates to multi-inncrional antibodies that recognise chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelates bound to an antigen recognition domain, where the metal chelate has a reactive functional group of complementary reactivity to the has a reactive functional group of complementary reactivity to the carctive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a covalent bond between the reactive site of the antibody and the carctive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody complex. Or addition of the metal chelate, a cell-mutant antibody complex. Or addition of the metal chelate, a cell-mutant antibody complex. Or addition of the metal chelate, a cell-mutant antibody complex. Or addition of the metal chelate, a cell-mutant antibody magnetic cresonance imaging, lanthanide luminescence, gamma-emissions or single cresonance imaging, lanthanide luminescence, gamma-emissions or single creating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide is the mutant protein sequence comprising a chimeric mutine antibody 2D12.5 creatible heavy chain protein fused to the human anti-tetamus toxin antibody can have an antibody chain constant region (20MH-TCRI) with NBTD and G54C mutantible heavy chain constant region (20MH-TCRI) with man exemplification metals or mutantion and a V5 epitope with (His)6 tag, given in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric murine 2D12.5 VH antibody fused to human TTCH protein with tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine; mouse; chimeric; human; TTCH; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission comography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; V5 epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                      invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 58.5; DB 8; Length 254; 59.1%; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ98108 standard; protein; 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KGELEGLPIPNPLL----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2004; 2004WO-US001808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2003; 2003US-00350555.
22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corneillie T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004065569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD098108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             His tag
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Novel human receptor activator of NFkappaB (hRANK) or human osteoprotegetin (hopg) variant polypeptides which bind to RANK ligand (RANKL) with equivalent binding affinity as hRANK or hOpg, useful for treating osteoporosis.

(MAXY-) MAXYGEN HOLDINGS LTD.

Haaning JM, Halkier T; WPI; 2002-691592/74.

N-PSDB; ABS56350

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chelating agents and metal chelates, particularly macrocyclic metal chelating agents and metal chelates, particularly macrocyclic metal chelates Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate has a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a contained of contained amino acid e.g. the "SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the reactive functional group of the metal chelate. The present invention chescribes using these antibodies for in vivo imaging where the antibody complex. Or surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody—metal chelate complex. On addition of the metal chelate, a cell-antibody—metal chelate complex. CC resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit correction and immunospapers activities. This polypeptide sequence is a chimeric murine antibody 2D12.5 variable heavy chain protein fused to haven in an exemplification of the
                                                                           Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                     invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG; RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy; osteoporosis; bone disease; human; pYhOPGb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 58.5; DB 8; Length 254; 59.1%; Pred. No. 0.58; ive 1; Mismatches 3; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble human OPG protein encoded by vector pYhOPGb.
                                                                                                                                                                                Disclosure; SEQ ID NO 85; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 RGPFEGKPIPNPLLGLDSTRTG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KGELEGLPIPNPLL ----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG71834 standard; protein; 338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2001; 2001DK-00000214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2001; 2001US-0267843P.
23-MAR-2001; 2001DK-00000498.
23-MAR-2001; 2001US-0278320P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2002; 2002WO-DK000090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 59.1
13; Conservative
                  2004-580725/56.
                                                                                                                                      autoimmune diseases.
                WPI; 2004-580725/
N-PSDB; ADQ98101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200264782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG71834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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This invention relates to a novel polypeptide having an amino acid
sequence that is different from and is at least about 70% identical to
the amino acid sequence of human receptor activator of NPKappaB (hRANK)
or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
(ligand (RANKL) that is at least as high as the binding affinity of hRANK
or hOPG to RANKL, as determined by functional competition assay. The
protein of the invention may have osteopathic activity and may act as a
RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
inhibitor. The nucleotide sequence shown in the invention may be used in
CG gene therapy. The protein of the invention or fusion proteins comprising
this protein are useful as a pharmaceutical, and in the preparation of a
CM medicament for treating or preventing osteoporosis, or other bone
can ediseases or diseases associated with binding of RANKL to the RANK
cerceptor. A host cell containing a vector expressing the protein is
cuseful for producing a polypeptide having binding affinity to RANKL,
where the polypeptide comprises at least one N- or O-glycosylation site
cand the host cell is a eukaryotic host cell capable of in vivo
cglycosylation, and/or the polypeptide is subjected to conjugation to a
cnon-polypeptide moisty in vitro. The protein of the invention has
conjugation and cell in vivo half-life and/or serum half-life comparated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRANK or hOPG and has an improved binding affinity to RANKL compared to the binding affinity of hRANK or hOPG to RANKL, as determined by a functional competition assay. The present sequence represents a soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG; RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy; osteoporosis; bone disease; human; pYhRANKD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numan OPG protein which is expressed on the surface of yeast cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein expressed by human RANK expression vector pYhRANKb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 58.5; DB 59.1%; Pred. No. 0.79; Live 1; Mismatches
                                                                                                                                                                                                                                                     Disclosure; Fig 15; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 RGPFEGKPIPNPLLGLDSTRTG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG71826 standard; protein; 349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGELEGLPIPNPLL----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2002; 2002WO-DK000090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200264782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG71826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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01-OCT-2002; 2002WO-DK000651.
                                                                                                           2001DK-00001433
                                                                                                                               11-OCT-2001; 2001US-0328896P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 59.1 es 13; Conservative
                                                                                                                                                                                                                    Terry BR, Nielsen SJ;
                                                                                                                                                                                                                                                               WPI; 2003-430211/40.
                                                                                                                                                                             (BIOL-) BIOLMAGE AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 368 AA;
                                                                                                                                                                                                                                                                                      N-PSDB; ACC72603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200037641-A2
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                                                                                                           01-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JAN-2001
                    10-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor. The nucleotide sequence shown in the invention may be used in gene therapy. The protein of the invention or fusion proteins comprising this protein are useful as a pharmaceutical, and in the preparation of a medicament for treating or preventing osteoporosis, or other bone diseases or diseases associated with binding of RANKL to the RANK receptor. A host cell containing a vector expressing the protein is useful for producing a polypeptide having binding affinity to RANKL, where the polypeptide comprises at least one N. or O-glycosylation site and the host cell is a enkaryotic host cell capable of in vivo glycosylation, and/or the polypeptide is subjected to conjugation to a con-polypeptide moietry in vitro. The protein of the invention has increased functional in vivo half-life and/or serum half-life compared to hRANK or hOPG and has an improved binding affinity to RANKL compared to the binding affinity of hRANK or hOPG to RANKL, as determined by a functional competition assay. The present sequence represents a human RANKL protein-HIS tag fusion protein encoded by the pyhRANKO expression vector used in teh method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence that is different from and is at least about 70% identical to the amino acid sequence of human receptor activator of NFKappaB (hRANK) or human osteoprotegerin (hOPG), and which has a binding affinity to RANK ligand (RANKL) that is at least as high as the binding affinity of hRANK or hOPG to RANKL, as determined by functional competition assay. The protein of the invention may have osteopathic activity and may act as a RANKL-mediated osteoclast activity
                                                                                                                                                                                                                                                                                   Novel human receptor activator of NFkappaB (hRANK) or human osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel polypeptide having an amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; heterologous conjugate; intracellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human amino acid sequence SEQ ID NO: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 6; 129pp; English.
                    09-FEB-2001; 2001DK-00000214.
09-FEB-2001; 2001US-0267843P.
23-MAR-2001; 2001US-0000498.
23-MAR-2001; 2001US-0278320P.
                                                                                                                                 (MAXY-) MAXYGEN HOLDINGS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 59.1
Watches 13; Conservative
                                                                                                                                                                             Haaning JM, Halkier T;
                                                                                                                                                                                                                                                                                                                                                          treating osteoporosis.
                                                                                                                                                                                                                        WPI; 2002-691592/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aeguoria victoria.
                                                                                                                                                                                                                                               N-PSDB; ABS54847.
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WO2003029827-A2

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                                                                                                                                                  The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular proteins. The present sequence is used in the
Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regularcy; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue reppir; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%; Score 58.5; DB 6; Length 368; 59.1%; Pred. No. 0.86;
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                                                                                                           Disclosure; Page 110; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 RGPFECKPIPNPLLGLDSTRTG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB10639 standard; protein; 374 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the invention
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18-MAR-1999;
08-NOV-1999;
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This invention describes a novel vascular endothelial growth factor-X

(VEGF-X) protein (Ia) and its encoding polymuclecide (IIa) which has

vulnerary, cytostatic, antirheumatic, antiarthritic, antipaoriatic and

antidiabetic activity and acts as an angiogenesis and vascularization

capilator. An antisense molecule of the invention is useful for treating

cor preventing cancer, rheumatoid arthritis, psoriasis and diabetic

cor preventing cancer, rheumatoid arthritis, psoriasis and diabetic

cor preventing cancer, rheumatoid arthritis, psoriasis and diabetic

cor preventing cancer, rheumatoid arthritis, psoriasis and diabetic

cor preventing cancer, rheumatoid arthritis, psoriasis and diabetic

vascularization including formation and proliferation of new blood

cor preparing medicaments for treating wounds such as dermal ulcers,

pressure sores, venous sores, diabetic ulcers and burns and to promote

skin graft growth, tissue repair, proliferation of new blood vessels,

tissue regeneration and organ repair by promoting angiogenic activity or

vascularization. This sequence represents a human VEGF-X protein which

can be expressed in mammalian systems and which is described in the

method of the invention
                                                                                                                                                                                                                               preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds.
                                                                                                                                                                                                       New vascular endothelial growth factor protein, useful for treating or
                                                    Yon JR, Dijkmans JJH, Gosiewska A;
                                                                                                                                                                                                                                                                                                         Disclosure; Fig 19; 127pp; English.
                                                    Sprengel JJ,
(JANC ) JANSSEN PHARM NV
                                                                                                                           2000-442669/38
                                                                              Xu J;
                                                                                                                                                     N-PSDB; AAA71983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 374 AA;
                                                                            Dhanaraj SN,
                                                 Gordon RD,
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2 65.0%; Score 58.5; DB 3; Length 374; 59.1%; Pred. No. 0.87; 3; Indels rred. NO. 0.87 1; Mismatches 347 RGPFEGKPIPNPLLGLDSTRTG 368 --RTG 17 Local Similarity 59.1 les 13, Conservative 1 KGELEGLPIPNPLL-Query Match Best Loca Matches 셤 ઠે

Gaps

AAE11082 standard; protein; 473 AA

AAE11082;

(first entry) 18-DEC-2001 C-terminal tagged rat delta-6-desaturase (rD6D-1).

Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema; mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection; gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome; endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome; cardiovascular disease; Crohn's disease; congenital liver disease; schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer; arterial hypertension; atherosclerosis; chronic inflammatory disorder; autoimmune disorder; hypercholesterolaemia; atopic disorder; rD6D-1; gene therapy; rat

Rattus sp

468. .473 /note= "6xHis tag" /note= "V5 tag" Region Region

Location/Qualifiers

WO200170993-A2

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The invention relates to polynucleotides that control delta-6 desaturase genes (D6D) and methods useful for identifying compounds which inhibit or promote the activity of mammalian D6D. Compounds which modulate D6D gene segments are useful for treating lipid metabolism disorders e.g. atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, cardiorders, viral infections and post viral fatigue, premenstrual syndrome, endometriosis, cystic fibrosis, alcoholism, alzheimer's syndrome, cardiovascular disease, Crohn's disease, cancer, congenital liver disease, schizophrenia, diabetes and diabetic complications including diabetic neuropathy, nephropathy and retinopathy. Compounds of the invention are also useful for inhibiting progressive and autoimmune disorders, hypercholesterolaemia and other atopic disorders. D6D genes are useful in gene therapy. The present sequence is C-terminal tagged rat delta-6-desaturase (rD6D-1) enzyme
                                                                                                                                                                                                                                                     Nucleic acid encoding delta-6-desaturase gene useful for treating atopic eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, gastrointestinal disorders, viral infections and post viral fatigue.
                                                                                                                                                                         De Antueno RJ;
                                                                                                                                                                         Ponton A,
                                                                                                                                                                       Smith HL, Allen SJ,
                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 5; 164pp; English.
                                          26-MAR-2001; 2001WO-CA000398
                                                                                24-MAR-2000; 2000CA-02301158
                                                                                                                            (SCOT-) SCOTIA HOLDINGS PLC.
                                                                                                                                                                                                                 WPI; 2001-611507/70.
27-SEP-2001
                                                                                                                                                                     Winther MD,
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65.0%; Score 58.5; DB 4; Length 473; 59.1%; Pred. No. 1.1; Live 1; Mismatches 3; Indels 5 1 KGELEGLPIPNPLL----RTG 17 Conservative Similarity Local Sim Query Match Matches 8

Sequence 473 AA;

Gaps

2,

completed: May 27, 2005, 13:43:56 : 8.45203 secs Search cor Job time

446 RGPFEGKPIPNPLLGLDSTRTG 467

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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/124,967
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1068, A
1068, A
3, Appli
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104, Appl
107, A
13536, A
13536, A
8827, A
99, Appli
4, Appli
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-213-808-25
US-09-213-808-25
US-09-318-8770-25
US-09-345-814-32
US-09-345-814-32
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US-09-345-814-32
US-09-345-814-32
US-09-349-016-10058
US-09-949-016-10069
US-09-949-016-10048
US-09-352-171-14
US-09-342-173-3
US-09-340-016-9104
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US-08-991-408-4
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US-08-991-408-3
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Gapop 10.0 , Gapext 0.5
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02142122481204820 0204481204820 0308077 0308077 0304487744458	CANCERS	Сарв
sedneuce Sed	RELATED : Synthe	Length 146; ; Indels 10; ACTOR-X
US-09-285-385C-20 US-09-902-540-15897 US-09-134-000C-4038 US-10-132-920B-2 US-09-70-69C-2 US-09-70-69C-2 US-09-70-69C-2 US-09-794-422-34 US-10-132-920B-27 US-10-132-920B-27 US-09-794-422-6 US-09-794-422-6 US-09-794-422-6 US-09-794-422-8 US-09-794-422-8 US-10-116-370-02 US-09-794-422-8 US-09-794	LIGNMENTS DIAGNOSIS OF 923,304 Artificial S	59; DB 4; No. 0.06; 1 G 17 G 17 G 140 G 140 G 140 G 33
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	pplicat: 97471 MATION: MATION: JIANG, I ENITON: CE: UTON: O ID NOW CENTIN I	Ouery Match Best Local Similarity 59.3%; Pred. No Matches 16; Conservative 0; Mismaches 16; Conservative 0; Mismaches 16; Conservative 0; Mismaches 16; Conservative 0; Mismaches 18; Conservative 0; Mismaches 18;
	SULT 1 -09-923-304-9 -09-923-304-9 Patent No. 67 GENERAL INFOR APPLICANT: TITLE OF INV FILE REPERAN CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL CURRENT APPL FEATURE: PRI FEATURE: OFTHER COTHER INFORM OTHER INFORM OTHER INFORM	-09-923-304-9 Query Match Best Local Simil Best Local Simil Batches 16; C 1 KGEL 14 KGEL 14 KGEL 19 Ap Betent No. 67839 GRERRAL No. 67839 GRERRAL NO. 67839 GRERRAL SPLICANT: Spr APPLICANT: Spr APPLICANT: Gord APPLICANT: OA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: DA APPLICANT: TOA CURRENT APPLICATION FILE OF INVENT FILE OF INVENT FILE OF STILING CURRENT APPLICATION DEALOR APPLIC
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ORGANISM: Artificial Sequence
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US-09-883-096-5
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APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pulley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 669
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Sequence 25, Application US/09328877D
Sequence 25, Application US/09328877D
Sequence No. 6730778
GRIERLI INFORMATION.
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjoin Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877D
GURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                        DB 4; Length 374;
                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                   Query Match 65.0%; Score 58.5; D
Best Local Similarity 59.1%; Pred. No. 0.2;
Matches 13; Conservative 1; Mismatches
PRIOR FILING DATE: 1999-03-18
PRIOR PELION NUMBER: US 60/164,131
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 130
SEGTWARE: Patentin version 3.2
SEQ ID NO 118
LENGTH: 374
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                                                                                                                                                                                                                                                                                                                                                                    1 KGELEGLPIPNPLL----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/09213888A Patent No. 6638731 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KGELEGLPIPNPLL----RTG 17
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ORGANISM: Artificial Sequence
                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-468-647A-118
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US-09-328-877D-25
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LENGTH: 669
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TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGH: 635
TYPE: PRT
ORGANISM: Tagged Ctenocephalides felis
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: V5HIS tagged
OTHER INFORMATION: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craven, Andrew
APPLICANT: Yu, Ming
APPLICANT: Sakowicz, Roman
APPLICANT: Patel, Umesh A.
APPLICANT: Davies, Katherine A.
APPLICANT: Patel, Willer A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
APPLICANT: Patel, Umesh A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                               Query Match 65.0%; Score 58.5; DB 4; Length 669; Best Local Similarity 59.1%; Pred. No. 0.39; Matches 13; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
IENGTH: 383
TYPE: PRT
                                                                                                                                                                                                                                                                                  1 KGELEGLPIPNPLL----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/09545814; Patent No. 6416977; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 KLEGKPIPNPLLGLDSTRTG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09883096
Patent No. 6680369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ELEGLPIPNPLL ----RTG 17
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APPLICANT: Beraud, Christophe
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651 EGEVKGGPEPTPLVQT 666
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                            8; Conservative
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   FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-489-039A-10689
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                               US-09-949-016-10058
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US-08-866-650-3
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                  Gaps
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                                Score 51.5; DB 4; Length 635; Pred. No. 4.8; 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/756,250
FILING DATE: 19910909
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,427
FILING DATE: 08 MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 45; DB Best Local Similarity 50.0%; Pred. No. 63; Matches 8; Conservative 5; Mismatches
                                                                                                                 612 EGKPIPNPLLGLDSTRTG 629
                                                                                                5 EGLPIPNPLL ----RTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REPERENCE/DOCKET NUMBER: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||::| | | ||::|
643 EGEVKGGPEPTPLVQT 658
                                57.2%;
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                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-07-756-250-16
                                Query Match
Best Local Similarity
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US-09-545-814-32
                                                                Matches
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVEXTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVEXTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVEXTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVEXTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10689

LENGTH: 410

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10689
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Pred. No. 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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Patent No. 5939321
GENERAL INPORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
46;
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Pred. No. 46;
2; Mismatches
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SMUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 10058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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STREET: 1 South Pinckney Street
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Gaps

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Query Match
48.9%; Score 44; DB 3; Length 1013;
Best Local Similarity 56.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                 Query Match
48.9%; Score 44; DB 2; Length 1013;
Best Local Similarity 56.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 5; Indels
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Sequence 14, Application US/09352171
Sequence 11, Application US/09352171
GENERAL INFORMATION:
APPLICANT: Rubin, Richard A
APPLICANT: Conway, Bruce
APPLICANT: Giuliano, Kenneth A
APPLICANT: Goodph, Albert H
APPLICANT: Dunlay, R. Terry
TITLE OF INVENTION: A System for Cell Based Screening
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Grahafar, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRIE BADABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/240,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09240473 Patent No. 6297011
                                                                                                                                                                                                                        846 GRLCGSKIPDPLMATG 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 GRĽCGSKÍPDPĽMAŤG 861
                                                                                                                                                                                            2 GELEGLPIPNPLLRTG 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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US-09-021-287-3
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US-09-240-473-3
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1.2e+02;
... 5; Indels
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US-09-021-287-3
Sequence 3, Application US/09021287
Sequence 3, Application US/09021287
Patent No. 5981717
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,650
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-500
TELEPAX: 608-251-9166
INFORMATION FOR SQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: READABLE FORM:
COMPUTER: PACENTEN PC-DOS/MS-DOS
SOFTWARE: PACENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,287
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Pred. No. 1.2e+02
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELEPHONE: 608-251-5000
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative 7
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-866-650-3
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 Sout
CITY: Madison
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; Sequence 9104, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR PLLING DATE: 2000-10-20
; PRIOR PAPLICATION NUMBER: 60/241, 755
; PRIOR PLLING DATE: 2000-10-03
; PRIOR PLLING DATE: 2000-10-03
; PRIOR PLLING DATE: 2000-10-03
; PRIOR PLLING DATE: 2000-10-03
; PRIOR PLLING DATE: 2000-10-03
; PRIOR PLLING DATE: 2000-10-03
; WINBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESE FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60778, Application US/09270767
Sequence 60778, Application US/09270767
GENERAL INFORMATION:
JENERAL INFORMATION:
JENERAL INFORMATION:
JELEOF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
JELEOF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
JELEOF INVENTION: NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
JOHNHARE: Patentin Ver. 2.0
JENOTH: 271
JENOTH: 271
JENOTH: 271
JTYPE: RRT
ORGANISM: Drosophila melanogaster
US-09-270-767-60778
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Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                        Score 43; DB 4; Length 14;
Pred. No. 1.6;
0; Mismatches 1; Indels
FILE REPERENCE: 97,022-D1
CURRENT APPLICATION NUMBER: US/09/352,171
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 14
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%; Prv
Matches 8; Conservative 0;
                                                                                                                                                                                                                                            ; OTHER INFORMATION: epitope tag
US-09-352-171-14
                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 58.3
Matches 7; Conservative
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14 GYPLPGPLAQTG 25
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1 GKPIPNPLL 9
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US-09-270-767-60778
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LENGTH: 622
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 27, 2005, 13:28:55; Search time 3.73348 Seconds (without alignments) 2331.700 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-622-893A-4 90 1 KGELEGLPIPNPLLRTG 17

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

50.0 757 1 VKGC_MOUSE Q981AN Q981AN BEGULLUS 50.0 758 1 VKGC_BOVIN Q07175 bos taurus 50.0 758 1 VKGC_HUMAN P38435 homo sapien 50.0 758 1 VKGC_RT Q08436 rattus norv 50.0 758 2 Q9GL59 Q9GL59 ovis aries
.0 758 1 VKGC_BUVIN QU/1/5 .0 758 1 VKGC_RAT 088495 .0 758 2 Q9GL59 Q9G159

Q9cp13 pasteurella Q6bza3 debaryomyce		P14268 canine aden O7m6a0 canine aden		Q7u384 bordetella	Q7u374 bordetella	Q7u361 bordetella	w		=	Q8pa76 xanthomonas
FTSK PASMU Q6BZA3	P73337 07UY62	HEX9 ADECT	067106	TRMD BORBR	TRMD_BORPA	TRMD_BORPE	Q543 <u>6</u> 0	Q67SK7	Q8TQC9	Q8PA76
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930	1371	103	145	257	257	257	266	275	339	482
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45	45 44.5	4 4	44	44	44	44	44	44	44	44
32	34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 08-W23 AC 08-W23 AC 08-W23 AC 08-W23 DT 01-OCT-2002 (TTEMBLEAL 22, Lat DT 01-OCT-2002 (TTEMBLEAL 26, Lat DT 01-OCT-2002 (TTEMBLEAL 26, Lat DT 01-OCT-2002 (TTEMBLEAL 26, Lat DT 01-WAR-2004 (TTEMBLEAL 26, Lat DT 01-WAR-2004 (TTEMBLEAL 26, Lat DT 01-WAR-2004 (TTEMBLEAL 26, Lat DT 01-WAR-2004 (TTEMBLEAL 26, Lat DT 01-WAR-2004) RN NCBI_TAXID=10548; RN Adhikary A.K., Matsuno S., Okabb RN Anhkary A.K., Matsuno S., Okabb RN Anhkary A.K., Matsuno S., Okabb RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN Anhkary A.K., Matsuno S., Okab RN A.Colog (TTEMBLEAL 23, Lat DT O1-WAR-2003 (TTEMBLEAL	SULT 1 JUA23 QBJW23 QBJW23 QBJW23 O1-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 26, E3 14.9kDa. Human adenovirus type 34. Viruses; dBDW viruses, no RNCBI_TAXID=10548; [1] SEQUENCE FROM N.A. STRAIN-Compton; PubMed=14693847; Adhikary A.K., Inada T., Nummukovyama A., Matsuno S., OK "Characterization of hexon adenovirus involved in epided J. Clin. Pathol. 57:95-97(20) EMBL; AB07924; BAC07480.1; InterPro	QBB855 QBB85, QBB85, QBB85, QBB85, QBB82, QBBR7, QB
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SEQUENCE FROM N.A. STRAIN=Holden;
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                                                                                                                       PIR; G64131; G
TIGR; HI1592;
                                                                                                                                                                                                                             DNA-binding
                                                                                                                                                                                                                                                                   SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Probable DNA motor protein. May track DNA in a ATP-dependent manner by generating positive supercoils in front of it and negative supercoils behind it (By similarity).

MISCELLANEGUS: Although strongly related to firsk, it lacks the typical transmembrane domains located at the N-terminal part of
                                                  Mei Y.F., Skog J., Lindman K., Wadell G.;
"Comparative analysis of the genome organization of human adenovirus
11, a member of the human adenovirus species B, and the commonly used
human adenovirus 5 vector, a member of species C.";
J. Gen. Virol. 84:2061-2071(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Wtierback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
[2]
SEQUENCE FROM N.A.
STRAIN=Slobitski,
MEDLINE=22749818; PubMed=12867636; DOI=10.1099/vir.0.19178-0;
                                                                                                                                                                                                            MEDLINE=22935380; PubMed=14573794; DOI=10.1099/vir.0.19497-0; Davison A.J., Benko M., Harrach B.; "Genetic content and evolution of adenoviruses."; "Genetic content and evolution of adenoviruses."; EMBL; AX163756; AAN62494.1: -... EMBL; AX532578; AAN62494.1: -... EMBL; BK001453; DAA01668.1: -... EMBL; BK001453; DAA01668.1: -... EMBL; PK009206 Adeno_E3. Pfam; PR06040; Adeno_E3. Pfam; PR06040; Adeno_E3. SEQUENCE 131 AA; 14966 MW; GEAE3911AAD51FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 131;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                             STRAIN=Slobitski;
Mei Y.-F., Skog J., Lindman K., Wadell G.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2004 (Rel. 45, Last amnotation update)
DNA translocase ftsK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 AA.
                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=ftsK; OrderedLocusNames=HI1592;
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                 2 GELEGLPIPNPLLRTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                          77 GELOGLPTENPWVEAG 92
                                                                                                                                                                                                                                                                                                                                                              55.6%;
                                                                                                                                                                                                                                                                                                                                                                           56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 56.2 les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTSK HAEIN
P45264;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage, by and for commercial
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                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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STRAIN=35p;
MEDLINE=22741997; PubMed=12857895;
MDDI=10.1128/JVI.77.15.8263-8271.2003;
Vogels R., Zujidgeest D., Van Rijnsoever R., Hartkoorn E., Damen I., De Berhune M.P., Koostense S., Penders G., Helmus N., Koudstaal W., Cecchini M., Wetterwald A., Sprangers M., Lemckert A., Ophorst O., Koel B., Van Meerendonk M., Quax P., Panitti L., Grimbergen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSÍTE; PS50901; FTSK; 1.
ATP-binding; Cell division; Chromosome partition; Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenovirus type 35.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Score 50; DB 1; Length 529; 53.3%; Pred. No. 29; 1:ve 3; Mismatches 4; Indels
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Basler C.F., Flomenberg P.F., Chen M., Horwitz M.S.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 387 FtsK.
191 198 ATP (Potential).
529 AA; 58767 MW; 0C0F882EADFE726D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q67729; Q77929;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
15.0 kDa protein (E3 15.0K protein) (16.1K protein)
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                                                                                                                                                                                                                                                                                                                                                                   TIGR; HI1592; -.
HAMAP; MF_01809; atypical; 1.
InterPro; IPR002643; FtsK_SpoIIIE.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
Pfam; PF01580; FtsK_SpoIIIE; 1.
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MEDLINE=22890078; PubMed=14528318;
Gao W., Robbins P.D., Gambotto A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Gene Ther. 10:1941-1949(2003).
                                                                                                                                                                                                                                                                                        EMBL; U32833; AAC23240.1; -. PIR; G64131; G64131.
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286 EAMCMPVPNPIWRLG 300
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Les 8; Conservative
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136 DGQPLPNPLQRAG 148

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Bout A., Goudsmit J., Havenga M.; "Replication-deficient human adenovirus type 35 vectors for gene transfer and vaccination: efficient human cell infection and bypass of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                              Score 48; DB 2; Length 131;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                     Pfam; PF06040; Adeno E3; 1. SEQUENCE 131 AA; 14974 MW; E4869B881FC9F743 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XCC3651.
OrderedLocusNames=XCC3651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA
                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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01-OCT-2002 (TrEMBLrel. 22, Last seq
                                                                         preexisting adenovirus immunity.";
J. Virol. 77:8263-8271(2003).
EMBL; U32664; AAA75324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:459-463(2002).
EMBL; AE012486; AAM42921.1; -.
HSSP; P14930; LLLD.
InterPro; IPR002579; MarB.
InterPro; IPR011057; M884_like.
Pfam; PF01641; SelR; 1.
                                                                                                                                                                                                    PIR; JC4767; JC4767.
InterPro; IPR009266; Adeno_E3.
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TIGRFAMB; TIGR00357; DUF25; 1.
                                                                                                                                                  EMBL; AY128640; AAN17492.1; -. EMBL; AY271307; AAP92358.1; -.
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56.2%;
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Best Local Similarity 56.27
Best Local 9; Conservative
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Du H., Minx P., Abbott A., Doebber A., de la Bastide M., Spiegel L.,

Nascimento L., Preston R., Kirchoff K., King L., Vil M.D., Baker J.,

Zutavern T., Sancos L., Bell M., Miller B., Kuit K., Rodriguez S.,

Cunnius D.M., Balija V., Shah R., Bahret A., O'Shaughnessy A.,

Palmar L., Yang C., Dedhia N., McCombie W.R.; databases.

Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                  Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017073; AAP52859.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 147;
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147 AA; 16177 MW; 7CF958DEE5551325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    147 AA; 16177 MW; 7CF958DEE5551325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              52.2%; Score 47; DB 2;
60.0%; Pred. No. 22;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.2%; Score 47; DB 2; 60.0%; Pred. No. 22; tive 2; Mismatches
                              147 AA
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                                                          Created)
                            PRT;
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                                                         01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KGELEGLPIPNPLLR 15
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ORFNames=OSJNBb0036B06.22;
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 9; Conservative
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                              PRELIMINARY;
                                                                                                     Putative retroelement. Name=OSJNBb0036B06.22;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE 147 AJ
                                                                                                                                                                                                NCBI_TaxID=4530;
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SEQUENCE 147 A
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RESULT 6
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            Q94HT5
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35 KGGLRGLPVRSPTLR 49

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=95011606; PubMed=7926792;
Lincoln A.J., Williams S.C., Johnson P.F.;
"A revised sequence of the rat c/6bp gene.";
Genes Dev. 8:1131-1132(1994).
-!- FUNCTION: C/EBP is a DNA-binding protein that recognizes two different motifs: the CCAAT homology common to many promoters and the enhanced core homology common to many enhancers.
-!- SUBUNIT: Binds DNA as a dimer and can form stable heterodimers with C/EBP beta and gamma.
-!- SUBCELIULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the bZIP family. C/EBP subfamily.
                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGD; 2326; Cebpa.
InterPro; IPR004827; TF_bZIP.
SMARY; SM00381; BRLZ; II.
PROSITE; PS50217; BZIP; I.
PROSITE; PS00036; BZIP; I.
BROSITE; PS00036; BZIP BAIC; FALSE NEG.
3D-structure; Activator; Direct profein sequencing; DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of a recombinant copy of the gene encoding C/EBP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.2%; Score 47; DB 1; Length 358; 62.5%; Pred. No. 58; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLLMEB89092001; PubMed=2850264;
Landschulz W.H., Johnson P.F., Adashi E.Y., Graves B.J.,
McKnight S.L.;
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Leucine-zipper.
4DA8F112F6EA95D0 CRC64;
                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
CCAAT/enhancer binding protein alpha (C/EBP alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 253-269
                                                                    358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poly-Pro.
Poly-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37371 MW;
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SFAC; T00108; -.
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Matches 10; Conservative
                                                                STANDARD;
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317 3
358 AA;
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                                                                                                                                                                                                                                                                  Name=Cebpa;
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                                                                CEBA RAT P05554;
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;

A Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., A Ktlenk H.-P., Clayton R.J., Gwinn M.L., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., A Richardson D.L., Conschenbush J., Lee N.H., Sutron G.G., Gill S.R., A Fleischmann R.D., Quackenbush J., Lee N.H., Sutron G.G., Gill S.R., Rikness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J., Peterson S.N., Reich C.I., Worli L.K., Badger J.H., Glodek A., Deterson S.N., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Shou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A., Utterback T.R., D'Andrea K.P., Bowman C., Fulli C., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fulli C., A Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., A Mosee C.R., Venter J.C.;

The complete genome sequence of the hyperthermophilic, sulphatericucing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2; Length 522;
Pred. No. 87;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITÉ, PS00086, CYTOCHROME P450, UNKNOWN 1.
Heme, Monooxygenase, Oxidoreductase.
SEQUENCE 522 AA; 59676 MW; 28E604C091E88DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                         01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.

EMBL; AAAB01008823; EAA05550.1; -.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Pypothetical protein AF0243.
OrderedLocusNames=AF0243;
                                                                                                                                                     Name=agCG54096; ORFNames=ENSANGG0000010013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 AA.
                                   522 AA.
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Best Local Similarity 55...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00067; P450; 1.
PRINTS; PR00463; EP450I.
PRINTS; PR00385; P450.
                                       PRELIMINARY;
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                                                                                                                                                                                                                               NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                 AGCP10524.
                                       Q70GZ3
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RESULT 9
Q7QGZ3
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa
                                                                        NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=NCU06884.1
                                                                                                                                                                                                     Gramene; Q7XGI5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=OR74A;
                                                                                                                             chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                               0783G9;
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                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Nipponbare;
Spiegel L., de la Bastide M., Nascimento L., Kirchoff K., King L.,
Spiegel L., de la Baker J., Bell M., Zutavern T., Santos L.,
Miller B., Kuit K., Rodriguez S., Cunnius D.M., Balija V., Shah R.,
Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC078944; AAK92616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                            52.2%; Score 47; DB 1; Length 529; 72.7%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 579;
                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                              Complete proteome, Hypothetical protein.
SEQUENCE 529 AA; 60503 MW; 57E9FBC20D284BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1832D98496BE25EF CRC64;
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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(TrEMBLrel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
97:
                                                                                                                                                                                                                                                                                                                               579 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47;
Pred. No.
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InterPro, IPR005162; Retrotrans gag.
                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                               PRT;
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SEQUENCE 579 AA; 63293 MW;
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                                                                                                      EMBL; AE001089; AAB90990.1; -. PIR; C69280; C69280.
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Nature 390:364-370(1997).
                                                                                                                                                                                                                    Local Similarity 72.7
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KGGLRGLPVRSPTLR
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222 GEFEGVPRPNP 232
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                                                                                                                                                                                                                                                                                                                                                                                            Name=OSJNBa0089D15.27;
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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01-OCT-2003 (
01-OCT-2003 (
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                                                                                                                                                                                                              Query Match
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ID Q7
AC Q7
DT 01
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Calagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Blkins T., Engels R., Wand S., Nielsen C.B., Butler J., Bndrizzi M., Oui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Selitrennikoff C., Mayolor J.A., Braun E.L., Zelter A., Schulte U., Roy A., Foley K., Naylor J., Mancell E., Bielke C., Rudd S., Frishman D., Kamal M., Kamvysselis M., Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Part R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                           Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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-1- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                       "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AE017061; AAPS2277.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009057; Homeodomain_like.
InterPro; IPR005162; Retrotrans gag.
Pfan; PF03732; Retrotrans gag.
SEQUENCE 579 AA; 63293 MW; 1832D98496BE25EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                     The Rice Chromosome 10 Sequencing Consortium;
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EMBL, AARX010000409, EAA29995.1; -.
GO, GO.0003824; F.catalytic activity; IEA.
Interpro; IPR000379; Ser_estrs.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Science 300:1566-1569(2003)
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Best Local Similarity 60.00,
Best Local 9; Conservative
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Putative retroelement.
ORFNames=OSJNBa0089D15.27;
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SETRAINS=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtep P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.;
"A predator unmasked iffe cycle of Bdellovibrio bacteriovorus from a genomic perspective."
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WDDINIS=21608550; PubMed=11741193; DOI=10.1126/science.1066804;

WOOD D.W., Setubal J.C., Kaul R., Monks D.B., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bdellovibrio bacteriovorus.
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein Atu1054 (AGR C. 1946p).
OrderedLocunNames-AGR C. 1946, Atu1054,
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobianes,
Rhizobiacees, Rhizobium/Agrobacterium group; Agrobacterium.
                                                     Length 2039;
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Pred. No. 45;
                                                                                                        4; Indels
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2039 AA; 220637 MW; 62E6EAA1E02A38A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                Query Match 52.2%; Score 47; DB 2; L Best Local Similarity 64.3%; Pred. No. 3.7e+02; Matches 9; Conservative 1; Mismatches 4;
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BX842649; CAE79221.1; -.
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58.3%;
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01-JUN-2002 (TrEMBLrel. 21,
25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                              4 LEGLPIPNPLLRTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
OrderedLocusNames=Bd1327;
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Best Local Similarity 58.3°
---- 7; Conservative
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SEQUENCE 202 AA:
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SEQUENCE
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Q6MND1
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SCHEL, AE009035; AAK86862.1; -. EMBL, AE2706; AE2706.

PIR; E97488; E97488.
Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                     STRAIN=Cereon; MEDLINE=2160851; PubMed=11743194; DOI=10.1126/science.1066803;
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Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein, Complete proteome.
SEQUENCE 255 AA; 27291 MW; 5B329B22B9C43683 CRC64;
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42.9%; Pred. No. sc.,
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                                                                               Science 294:2317-2323(2001).
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68 EGDSDGIPLPDPLV 81
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Best Local Similarity
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SEQUENCE FROM N.A.
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GenCore version 5.1.6 Copyright (c). 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 27, 2005, 13:34:21 ; Search time 1.3049 Seconds (without alignments) 1253.491 Million cell updates/sec

1 KGELEGLPIPNPLLRTG 17 US-10-622-893A-4 90 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters;

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMAKIES	
Result No.	Score	Query Match	, Length	DB	OI.	Description
		7 33	603	;	264121	
10	9 4	7 6		10	174767	Ri gene encoding h
m	47	52.2	358	0	A54265	CCAAT/enhancer-bin
4	47	52.2		7	C69280	conserved hypothet
S	46	51.1		7	AE2706	conserved hypothet
9	46	51.1		7	E97488	hypothetical prote
7	45	50.0		7	AF3320	flavohemoprotein [
80	45	50.0		7	S51600	phosphorylase kina
0	45	50.0		~	A39283	gamma-glutamyl car
10	45	50.0		7	A47439	gamma-glutamyl car
11	45	50.0	-	~	S77521	sensory transducti
12	44	48.9		Н	SXADC2	hexon-associated p
13	44	48.9		~	G70384	hypothetical prote
14	44	48.9	3 266	~	S44954	1mbG protein - Str
15	43.5	48.3		N	н87699	conserved hypothet
16	43.5	48.3		~	T17462	disease resistance
17	43	47.8		~	H72538	hypothetical prote
18	43	47.8	3 222	н	MINIZSP	nonstructural prot
19	43	47.8		7	H75264	hypothetical prote
20	43	47.8		-	RRNZSP	polymerase-associa
21	43	47.8		7	T45685	hypothetical prote
22	43	47.8		~	B75191	probable ATP-depen
23	42.5	47.2		~	C39135	hypothetical prote
24	42	46.7		~	C81670	undecaprenyl pyrop
25	42	46.7		~	E71512	hypothetical prote
56	42	46.7		~	AG0700	probable pathogeni
27	42	46.7	322	~	E82505	conserved hypothet
28	42	46.7		7	S70357	forkhead transcrip
29	42	46.7	7 598	7	F83977	hypothetical prote

hypothetical prote	cranscription init	H+-exporting ATPas	nonstructural poly	phosphoribosylamin	type 4 prepilin pe	ribosomal protein	ATP-binding protei	psp operon transcr	NADH dehydrogenase	probable NADH dehy	4-hydroxybutyryl-C	Radi7 protein homo	aspartate-tRNA lig	hypothetical prote	excision repair pr
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ALIGNMENTS

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C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: G64131

Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: G64131 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-529 <TIGR> A;Cross-references: UNIPROT:P45264; GB:U32833; GB:L42023; NID:g1574432; PIDN:AAC23240.1; C;Superfamily: Bacillus subtilis DNA translocase spoIIIE

Gaps ; 0 Query Match 55.6%; Score 50; DB 2; Length 529; Best Local Similarity 53.3%; Pred. No. 4.3; Matches 8; Conservative 3; Mismatches 4; Indels

3 ELEGLPIPNPLLRTG 17 g ઠે

| |:|:||: | | 286 EAMGMPVPNPIWRLG 300

E3 gene encoding hypothetical 15.0k protein - human adenovirus 35
C;Species: Mastadenovirus h35 (human adenovirus 35)
C;Species: Jo-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JG4767
R;Basler, C.F.; Droguett, G.; Horwitz, M.S.
Gene 170, 249-224, 1996
A;Titler: Sequence of the immunoregulatory early region 3 and flanking sequences of adeno A;Reference number: JG4765; MUID:96235144; PMID:8666254
A;Accession: JG4767

A;Molecule type: DNA A;Residues: 1-131 <BAS> A;Cross-references: UNIPROT:Q67729; GB:U32664; NID:g984529; PIDN:AAA75324.1; PID:g984532

A,Gene: E3 C,Superfamily: adenovirus early E3 16K glycoprotein

ö Length 131; 6; Indels Query Match 53.3%; Score 48; DB 2; Best Local Similarity 56.2%; Pred. No. 1.8; Matches 9; Conservative 1; Mismatches

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Gaps

2 GELEGLPIPNPLLRTG 17

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conserved hypothetical protein Atul054 [imported] - Agrobacterium tumefaciens (strain C58 C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                     Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-255 <KUR>
A;Cross-references: UNIPROT:Q8UGI3; GB:AE008688; PIDN:AAL42067.1; PID:g17739446; GSPDB:GAA;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 2944, 2323–2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97159; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessci Proc. Natl. Acad. Sci. U'S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitenss A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q8UG13; GB:AE007869; PIDN:AAK86862.1; PID:g15156078; GSPDB:GP
                                                                                                                                                                                                                                                                                                                                                     ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004
C;Accession: AF3320
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68 EGDSDGIPLPDPLV 81
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A;Molecule type: DNA
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C69280
C;000served hypothetical protein AF0243 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69280
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson.; Flaischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Dieterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Dieterback, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Accession: C69280
A;Accession: C69280
A;Accession: C69280
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
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Kaesidues: 1-529 «KLE»
A;Cross-references: UNIPROT:029996; GB:AE001089; GB:AE000782; NID:g2689412; PIDN:AAB9099
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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CCAAT/enhancer-binding protein - rat

NyAlternate names: C/BBP

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C;Accession: S06890; A54265

R;Landschulz, W.H.; Johnson, P.F.; Adashi, E.Y.; Graves, B.J.; McKnight, S.L.

Genes Dev. 2, 786-800, 1988

A;Title: Isolation of a recombinant copy of the gene encoding C/EBP.

A;Reference number: S06890; MUID:89092001; PMID:2850264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A,Molecule type: DNA
A,Residues: 129, 'RLMLSPGRGPRAAPSPTCRPGAAGR',55-358 <LA2>
A,Cross-references: UNIPROT: P05554; EMBL: X12752
A,Cross-references: UNIPROT: P05554; EMBL: X12752
A,Note: the authors translated the codon AGC for residue 21 as Asp A,Note: this sequence has been corrected
A,Note: this sequence has been corrected
B,Lincoln, A.J.; Milliams, S.C.; Johnson, P.F.
Genes Dev. 8, 1131-1132, 1994
A,Title: A revised sequence of the rat C/EBP gene.
A,Reference number: A54265; MUID:95011606; PMID:7926792
A,Molecule type: DNA
A,Residues: 1-60 <LINA
A,Residues: 1-60 <LINA
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Pred. No. 13;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X12752
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Keywords: transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2;
Pred. No. 8.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GSLKGLAGPHPDLRTG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 52.2%;
Local Similarity 62.5%;
les 10; Conservative ;
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Best Local Similarity 72.7%;
Matches 8; Conservative
77 GELHGLPTENPWVEAG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||:| |||
GEFEGVPRPNP 232
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RESULT 5

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gama-glutamyl carboxylase (EC 4.1.1.-) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47439; A38199; B39283; C39283
R;Rehemtulla, A.; Roth, D.A.; Wasley, L.C.; Kuliopulos, A.; Walsh, C.T.; Furie, B.; Furi
Proc. Natl. Acad. Sci. U.S.A. 90, 4611-4615, 1993
A;Title: In vitro and in vivo functional characterization of bovine vitamin K-dependent
A;Reference number: A47439; MUD:93281629; PMID:8506307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule_type: mRNA
A;Residues: 1-758 cRRH-
A;Cross-references: UNIPROT:Q07175; GB:L09726; NID:g289398; PIDN:AAA30425.1; PID:g289399
R;Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.
R;Wu, C.M.; Cheung, W.F.; Annary 1992
A;Reference number: A38939
A;Accession: A38939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiKaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
Kheaidues 1-1371 cKAN3.
A;Cross-references: UNIRROT:P73337; EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA1736
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensory transduction histidine kinase sll1124 - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll1124
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Cloning and expression of the cDNA for human gamma-glutamyl carboxylase. Reference number: A39283; MUID:92086858; PMID:1749935
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A;Reaidues: 96-758 «WUA>
A;Cross-references: GB:M81593; NID:g162744; PIDN:AAA30410.1; PID:g162745
A;Cross-references: GB:M81593; NID:g162744; PIDN:AAA30410.1; PID:g162745
R;Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.
Science 254, 1634-1636, 1991
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A,Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 37-50 <WU3>
C;Keywords: carbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: B39283
Status: nucleic acid sequence not shown:
Molecule type: mRNA
                                       :||::| | ||::|
643 EGEVKGGPEPTPLVQT 658
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643 EGEVKGGPEPTPLVQT 658
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Conservative
      1 KGELEGLPIPNPLLRT
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A;Cross-references: GB:M81593
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Matches 8; Conserv
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Best Local Similarity
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                        A;Molecule type: DNA,
A;Residues: 1-378 «KUR».
A;Residues: 1-378 «KUR».
A;Residues: 1-378 «KUR».
A;Experimental source: UNIPROT: 08Y197; GB: AE008917; PIDN: AAL51729.1; PID: 917982465; GSPDB: GA: Experimental source: strain 16M
C;Genetics:
A;Gene: DME10548
A;Map position: I
C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
551600
phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster)
phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Aug-2004
C;Accession: S51600
R;Bahri, S.,, Chia, W
Mol. Genet. 245, S88-597, 1994
A;Title: DPhK-gamma, a putative Drosophila kinase with homology to vertebrate phosphory)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-560 <BAH>
A;Cross-references: UNIPROT:Q9VYV7; EMBL:U13014; NID:g531470; PIDN:AAA64560.1; PID:g5314
A;Note: the authors translated the codon CAT for residue 528 as Ala and CAC for residue
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-77 < WTD>
A;Cross-references: GB:M81592
C;Keywords: carbon-carbon lyase; carboxy-lyase
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R;Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.
Science 254, 1634-1636, 1991
A;Title: Cloning and expression of the CDNA for human gamma-glutamyl carboxylase.
A;Reference number: A39283; MUID:92086858; PMID:1749935
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C,Species: Homo sapiens (man)
C,Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 06-Dec-1996
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 560;
                                                                                                                                                                                                                                                                                              2; Length 378;
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Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                        50.0%; Score 45; DB 46.7%; Pred. No. 19; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Superfamily: protein kinase homology
C.Keywords: phosphotransferase
F;21-291/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: FlyBase:PhK-gamma
A;Cross-references: FlyBase:FBgn0011754
A;Map position: 10
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266 EISAVPVPSPLPETG 280
                                                                                                                                                                                                                                                                                                                                                                                                               3 ELEGLPIPNPLLRTG 17
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Best Local Similarity 72...
8; Conservative
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LQLPNPLLQTG 449
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Matches 8; Conserv
A;Status: preliminary
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Indels

3; Mismatches Score 44; Pred. No.

DB 2; Length 266;

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A;Cross references: UNIFROT:Q54360; EMBL:X79146; NID:g499194; PIDN:CAA55753.1; PID:g4876: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87699
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.!
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon;
n, J.; Ermolaeva, M.; Whithe, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:Q9A2D1; GB:AE005673; NID:g13425386; PIDN:AAK25596.1; GSPDB:GA
                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-266 <PE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein CC3634 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87699
                                                                                                                                                                                               A;Gene: 1mbG
C;Superfamily: Streptomyces lincolnensis 1mbG protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27, 2005, 13:48:46
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219 GEVPGIPVPPPAAR 232
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Best Local Similarity 50.0
Matches 7; Conservative
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Matches 9; Conserv
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Job time : 4.3049 secs
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  A;Accession: S69816
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SYADC2
Machology Inc.
Syabc2
C;Species: Mastadenovirus can2 (canine adenovirus 2)
Syabc2
A;Note: host Canis lupis familiaris (dog)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Date: 30-Sep-1990 #sequence of El region of canine adenovirus type 2.
N;Shibata, R.; Shinagawa, M.; Iida, Y.; Tsukiyama, T.
Virology 172, 460-467, 1989
A;Title: Nucleotide sequence of El region of canine adenovirus type 2.
A;Recession: D34165
A;Title: Nucleotide sequence of El region of canine adenovirus type 2.
A;Mocession: D34165
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
C;Superfamily: adenovirus hexon-associated protein (IX)
C;Keywords: hexon-associated protein
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G70384
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A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_978
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C;Species: Streptomyces lincolnensis
C;Species: Streptomyces lincolnensis
C;Species: Streptomyces lincolnensis
C;Accession: 569816; 844954
R;Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
R;Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
A)- Microbiol. 16, 1137-1156, 1395
A;Title: Molecular characterization of the lincomycin-production gene cluster of Strepton, R;Reference number: 569805; MUID:96020646; PMID:8577249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70384 A;Accession: G70384 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 6.1;
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  5; Indels
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Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                       1 KGELEGLPIPNPLLRT
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ELLGLPVPRPRLK 56
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Matches 7; Conservative
  8; Conservative
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A; Residues: 1-145 <AQF>
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2; Mismatches

Score 43.5; DB 2; Length 360; Pred. No. 31;

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May 27, 2005, 13:47:36 ; Search time 136.87 Seconds (without alignments) 1189.648 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Description	Sequence 5, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 53616, A	Sequence 14478, A	Sequence 412, App	Sequence 42701, A	Sequence 1, Appli	Segmence 68225. A
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QI	US-10-622-893A-5	US-10-622-893A-3	US-10-470-678-9	US-10-470-678-10	US-10-470-678-8	US-10-232-655-3	US-10-232-655-1	US-10-767-701-53616	US-10-156-761-14478	US-10-287-274-412	US-10-282-122A-42701	US-10-829-427-1	US-10-282-122A-68225
8	17	17	17	17	17	14	14	16	14	14	15	17	15
* Query Match Length DB	472	437	440	440	440	437	437	139	384	433	433	387	385
Query Match	100.0	92.1	45.6	45.6	45.5	24.8	23.7	8.3	7.3	9.9	9.9	9.9	6
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248 TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM- 306
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                                                     ASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDF
                                                                                                                                                                                                                    Sequence 9, Application US/10470678

Fublication No. US20050101771A1

GENERAL INFORMATION:

APPLICANT: KOUZUMA, Taktij et al.

TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS

FILE REFERENCE: 1514-0121P

CURRENT APPLICATION NUMBER: US/10/470,678

CURRENT APPLICATION NUMBER: US 2001/22953

PRIOR APPLICATION NUMBER: UP 2001/22953

PRIOR PILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-08-08

NUMBER OF SEQ ID NOS: 10

SSOTUMARE: Patentin version 3.2

LENGTH: 440
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Best Local Similarity 50.9%; Pred. No. 5.6e-103;
Matches 223; Conservative 75; Mismatches 133;
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ORGANISM: Artificial Sequence
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; LOCATION: (372)..(372)
US-10-470-678-9
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                                                        EAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKN
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Publication No. US20050014935A1

GENERAL INFORMATION:
APPLICANT: Yuan, Chong-Sheng
APPLICANT: Date, Abhijit
APPLICANT: Wang, Yuping
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
FILE REFERENCE: 466992001300
CURRENT APPLICATION NUMBER: US/10/622,893A
CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version 4.0
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// OTHER INFORMATION: 40%-100% identity to the amadoriase US-10-622-893A-3
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ORGANISM: Artificial Sequence
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US-10-622-893A-3
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                                                                                                                                        APPLICANT: KOUZUNA, Takuji et al.
TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P
CURRENT APPLICATION NUMBER: US/10/470,678
CURRENT ATLING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: UP 2001/22953
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-13
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%; Score 1152.5; DB 17; Length 440; 50.9%; Pred. No. 7e-103;
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75; Mismatches 133; Indels
                                                                                             ; Sequence 10, Application US/10470678; Publication No. US20050101771A1; GENERAL INFORMATION:
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NRVMDF--HDVKEWTNVQ 442
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; LOCATION: (372)..(372)
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RESULT 5 US-10-470-678-8 ; Sequence 8, Application US/10470678

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TADSKGDDEDSIWKALSYAAAQGWLHDPVFQPFCHNTGSVVAGSTPKSIKQL-VEDEIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:||:||:||:||:||:||:|||
180 KFITGSPEGKVESLIFEDGDVRGAKTADGKEHRADRTILSAGASAEFFLDFENQIQPTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 GOYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSIPFEKTQI PKEAETRVRALLKETMPQLADRPFSFARI CWCADTANREFLI DRHPQYHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVIS--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-PNLVELTRPEOFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10232655
Publication No. US20030157593A1
GENERAL INFORMATION
APPLICANT: KURCSAWA, KEIKO
APPLICANT: HIROKAWA, KOZO
APPLICANT: KALIYAWA, NAOKI
TITLE OF INVENTION: No. US20030157593A1e1 fructosyl peptide oxidase
FILE REFERENCE: 227590US0
GENERAL INFORMATION:
GENERAL INFORMATION:
TOTAL SOLUTION:
TITLE OF INVENTION: CANDENS TONE
FILE REFERENCE: 1516-0121P
CURRENT PEDLICATION NUMBER: US/10/470,678
CURRENT PEDLICATION NUMBER: US/10/470,678
CURRENT PEDLICATION NUMBER: UP 2001/2953
FRIOR APPLICATION NUMBER: UP 2001/39796
FRIOR PEDLICATION NUMBER: UP 2001/39796
FRIOR PEDLICATION NUMBER: UP 2001/39796
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 1151.5; DB 17; Length 440; 50.9%; Pred. No. 8.7e-103; Live 75; Mismatches 133; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic protein sequence of SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 NRVMDF--HDVKEWTNVQ 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.9%
Matches 223; Conservative
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 DTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 -GIRLRNGPDLO----LSLESLDMWQNDELFKPFFHQVGMIDCSSSKEGIENLRRKYQTL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 LQDKGVKFGFG-GAGTFQQPLFAADGKTCIGLETTDGTKYFADKVVLAAGAWSPTLVDLE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 NQLRPTAWILVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNM- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VQSADGTMMSIPFEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 SGQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSOEGLDRLGVRVRP- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 ----GEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAARE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 LDAGIGLEKTNVWLESEDEILAKAP-NFTREQVKGWKGLFCTDG-GWLAAAKAINAIGIF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AQRMGVKFVTGTPQGRVVTLIF--ENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LAVTKSSSLLIV--GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MINOMANA, KEIKO
APPLICANT: MINOKAWA, KEIKO
APPLICANT: HINOKAWA, KOZO
APPLICANT: HINOKAWA, KOZO
TITLE OF INVENTION: NO. USZOJOJOJSTS93ALel fructosyl peptide oxidase
TITLE OF INVENTION: NO. USZOJOJSTS93ALel fructosyl peptide oxidase
FILE REFERENCE: 227590USO
CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: JP 2001-378151
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-112
PRIOR APPLICATION NUMBER: JP 2001-378151
PRIOR PILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: JP 2002-228727
PRIOR APPLICATION NUMBER: JP 2002-228727
SPIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 24
CSOFTWARE: PATENTIN OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                Length 437;
                                                                                                                                                                                                                                                                                                                                              ch 24.8%; Score 627; DB 14; Length 4 il Similarity 34.1%; Pred. No. 9.2e-52; 153; Conservative 82; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 IAANRNWRDTLGRFGGPNRVMDFHDVKEW 438
CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: UP 2001-266665
PRIOR FILING DATE: 2004-09-04
PRIOR FILING DATE: 2001-31-12
PRIOR APPLICATION NUMBER: UP 2001-378151
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-08-06
NUMBER: OF SEQ ID NOS: 24
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 GDALRS-----RRGAPAK--DLAEMPGW 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/10232655; Publication No. US20030157593A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Eupenicillium terrenum
                                                                                                                                                                                                                                        437
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US-10-232-655-1
                                                                                                                                                                                                                                                                                                       US-10-232-655-3
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Best Local S:
Matches 153
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Sequence 53.65, Application US/10767701

Sequence 53.616, Application US/102684A1

GENERAL INFORMATION:
SAPPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT PRILIGATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 TPQGRVVTLIFENNDVK--GAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 -GAGSFKQPLFDDEGTTCIGVETADGTKYYADKVVLAAGAMSPTLVDLEDQCCSKAWYA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 MMSIPFEKTQIPKE-----AETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 IEVNEILAEEAFNGWKNDPLPKPYYHDTGLLMSACSOEGLDRLGVRVRPGEDPNL-VELT 136
                                                                                                                                                                                                                                                                                                                                                                                         137 R---PEQFRKLAPEGVLQGD-FPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 HIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQ-----SADGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 HIQLIPEEAAEYKGVPVVYNGEFGFFFEPN-EFGVIKVCDEFPGFSRFKEHQPYGAPSPK 301
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                                                                                                                                                                                                                                                                                                                           20 LLIVGAGTWGTSTALHLARRGY--TNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 HPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNP------
                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 8.3%; Score 210.5; DB 16; Length 139; Local Similarity 33.6%; Pred. No. 5.3e-12; nes 44; Conservative 21; Mismatches 39; Indels 27;
                                                                                                           Length 437;
                                                                                                                                                        86; Mismatches 162; Indels
                                                                                                           23.7%; Score 600; DB 14; 32.7%; Pred. No. 3.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: 13394327.pep
US-10-767-701-53616
                                                                                                           Query Match
Best Local Similarity 32.74
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 -- DIAANRNWR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 PKDLADMPGWK 432
LENGTH: 437
TYPE: PRT
ORGANISM: Coniochaeta sp.
                                                                     US-10-232-655-1
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Best Local S
Matches 44
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Query Match 6.6%; Score 168; DB 14; Best Local Similarity 23.0%; Pred. No. 4.1e-07; Matches 120; Conservative 59; Mismatches 176;
                                   Application US/10287274
5. US20030181408A1
                                 Sequence 412, Application US/1
Publication No. US20030181408A
GENERAL INFORMATION:
APPLICANT: FOYESTH, R. Allyn
                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Escherichia coli
US-10-287-274-412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-282-122A-42701
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375 GRGFKYLPSIGNLIVDAMEGKVPOKIHELIKWNPDIAANRNWRDTLG-----RFGGPNRV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AĞSLRSATQMDLPHEMLDAKEIRRRPPTLNPSNDEVALYEK------ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 QGDPPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TIERQVMYWFQPRHGVGPFR-PENHPIY--IWEDAEGVQVYGFPSIDGPDLGAKVAFFRK 273
                                 -----ROPRDDLGTEFOKKWSWPKOK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 EDPAYVPLLLRSYELYEEVERSTGREV-ATLSGGVMVGRPDSLTV------- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 PLFKPYYHDTGLLMSACS----QEGLDRLGVRVR-PGEDPNLVELTRPEQFRKLAPEGVL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------KAĞLVRPENMVAAHLQLATRQĞAE------LHFEEPMTRW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 AVTGDG-KIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 NIERG--FFFEPDEERGEIKICDEHPGYTNMVQSADGTMM------SIPFEKT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 QIPKEAET-----RVRALLKETMPQLADRPFSF--ARICWCADTANREFLIDRHPQY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VSPTYDVIVIGLGGMGSAAAHHLSARG---ARVLGLEKFGPVHNRGSSHGGSRITRQSYF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 -DPYPVPSAI-----SAGNDVNKVISSGQYSNNKDEIEVNEILAEEAFNGWKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 184; DB 14; Length 384;
; Pred. No. 9.4e-09;
60; Mismatches 139; Indels 158;
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                                                                                                                                                                                                                                                             APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADANOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TILE OF INVENTYON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14478
                                                                                                                                                                                            ; Sequence 14478, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Streptomyces avermitilis US-10-156-761-14478
                  7.3%;
                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 22.15
Matches 101; Conservative
                                                                                           107 YHFDHI--WTN 115
                                                                      MDFHDVKEWTN 440
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APPLICANT: Chleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Cyekind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
FITLE OF INVENTION: GENES. US/10/287,274
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVNKVISSGQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 -KICDEHPG----YTNMVQSADG-----TWMSIPFEKTQIPKEAETRVRALLKET-- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 GRICDDLPGGAFLYTNQQTLSLGIVCPLSSLTQSRVPASELLTRFKAHPAVRPLIKNTES 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 -----NSVLAERHGLV---TRPAGEAMALGIKEVLSLETSAIEERFHLENNEGAALLLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 --SKNLSGGRL-----YTHALAB------LLPQFHLTAPLERRITHESLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ---GVRVRPGEDPNLVELTRPEQFRKLAPEG----VLQGDFPGWKGYFARSGAGWAHARN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGGSGDDDDLALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 TPDGVTT------FSSLQPGGESWSVLRARFDPW----
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
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APPLICANT: FALTYAMA, NACKI
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, GENES AND RECOMBINANT DNAS THEREOF,
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, GENES AND RECOMBINANT DNAS THEREOF,
TITLE OF INVENTION: AND METHODS FOR PREPARING THE SAME
FILE REFERENCE: 25220205
CURRENT APPLICATION NUMBER: US/10/829, 427
CURRENT FILING DATE: 2004-04-25
PRIOR FILING DATE: 2003-11533
PRIOR FILING DATE: 2003-11-27
PRIOR FILING DATE: 2004-04-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 1
LENGTH: 387
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                                                         119 RLGVRVRPGEDPNLVELTRPEQFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAA 178
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                           374 SGRGFKY----LPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGG-PNR 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 VNEILAEEAFNGWKNDPLFKPYYHDTGLL------D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 KNQLRPTAWTLVHIALKP-----EERALYKN---IPV-IFNIERGFFFEPDEERGE
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                                                                                                                                                              375 LQRPGWYRTWPALM-QDISRDLWDQGDKPVP-PLRQLFWHH 413
                                                                                                                             429 VMDFHDVKEWINVQYRDISKLKGELEGLPIPNPLLRTGHHH 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Mismatches 173;
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6.6%; Score 166; DB 17;
Best Local Similarity 21.4%; Pred. No. 5.4e-07;
Matches 89; Conservative 68; Mismatches 173;
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COTHER INFORMATION: Synthetic Peptide US-10-829-427-1
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10829427
Publication No. US20050026265A1
GENERAL INFORMATION:
APPLICANT: FURUKAWA, KEISUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-10-282-122A-68225
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US-10-829-427-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----MPQ--LADRPFSFARICW------CADTANREFLIDRHPQYHSLVLGCGA 373
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                    APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 TPDGVTT-------FSSLQPGGESWSVLRARFDPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 168; 23.0%; Pred. No. 4
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                                                                                                                           Carr, Grant
Yamamoto, Robert
Forsyth, R.
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 23.0
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
                                                                         Daniel
                                                                                                       Trawick
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LENGTH: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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327 ILKETWPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGN 386
302 CVSRVFPDLIARPYA-SRKCVYTWTPDEAFIIGESKELPSVFYVSACSGHGFKFAPALGS 360
   252 EDGRILYGTPQIDNAEPGIKI----GFHNHQQSALDPRTQLEPASDAQIEE----1SA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 IEVN-EILAEEAFNGWKNDPLFKPYYHDTG--LLMSACSQEGLDRLGVRVRP--GEDPNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 INIRLGARSLEAFGRFGEEPGQDIGLHRVGYLFLLSTPEEVAAFETGVRLONSLGVPSRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 VELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 F----VTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCA------GASAGQF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 VLRHCEVTG-----IETRGDDITAVLTRRGRI--GTGTVICAAGAWSKAVGAMVGVD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 LDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGY 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 TINMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANRE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 L-----VGMSDPDETTGFSTETHDRWIPRLCEAMERRAPPLLDLRR-----TGGWA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 LPVRPLRRQIAVTEPVTGLPP-----GLPMTIDFTSSLYFH-----TEGPGL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ADVVVIGGGVMGTSIAYHLARAGVRDVVLVERDELASGSTSR-----AAGGVRAQFSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 FLIDRHPQYHSLV-----LGCGASGRGFKYLPSIGNLIVDAMEGKVP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 381;
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306 GLYEITPDHNALIGEAGSCSRFLYATGFSGHGFLQGPAVGEVIRDLYLDRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, HIROSHI
APPLICANT: BHRBA, TADAYOSHI
APPLICANT: SARRAI, YOSHIYUKI
APPLICANT: SARKXI, YOSHIYUKI
APPLICANT: APPLICANT: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9328, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptomyces avermitilis US-10-156-761-9328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                         387 LIVDAMEGK 395
                                                                                                                                                                                                                                                                                                             : |: |:
361 CLARALAGO 369
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR PILING DATE: 2000-03-21

PRIOR PELICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-26

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

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PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 PGEDPNLVELTRPEOFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAAREA--- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PQGRVVTLIFENNDVKGAV---TG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P----AKAG-GIAHOR--ITAAEVEARFS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 VFRADENMEAVFEGGAFTIAADDARLQMLNQAVAHGAQMRFGSHVQDITRVESEFLLRLS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 RQAYWEGSDYLS----LLAEADLGWRELQATSHRPLLHYSG--------GLFIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGKIWRAERTFLCAGAS-AGOFL-DFKNOLRPTAWTLVHIALKPEERALYKNIPV-IFNI
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23.5%; Pred. No. 6.7e-07;
tive 53; Mismatches 161; Indels 114;
Sequence 68225, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QRMGVKFVTGT----
                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas putida
US-10-282-122A-68225
                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 23.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2000-03-21

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PRIOR PELING DATE: 2000-05-23

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20.7%; Pred. No. 0.00017;
Live 63; Mismatches 147; Indels 134; Gaps
Sequence 55515, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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us-10-622-893a-5.rup

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 27, 2005, 13:28:55 ; Search time 103.659 Seconds (without alignments) 2331.700 Million cell updates/sec

score:

US-10-622-893A-5 2530 1 MGGSGDDDDLALAVTKSSSL.....LEGLPIPNPLLRTGHHHHHH Sequence:

472

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 of hits satisfying chosen parameters: Total number

1612378 seqs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match .0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			042629 aspergillus			Q92261 penicillium		-	Q765a8 coniochaeta	O43029 schizosacch	Q9utm9 schizosacch				-		bacillus		bacillus	Q9v9b5 drosophila	Q827h4 streptomyce	P40854 streptomyce	Q9p0z9 homo sapien		bacil				Q66in9 xenopus lae		Q6hill bacillus th
SUMMARIES	а	P78573	092204	042629	Q6BZB0	Q6BZA7	092261	Q96UT4	Q765A9	Q765A8	043029	Q9UTM9	075638	Q6CLI0	Q6BN43	Q6BN42	Q9P976	MSOX_BACB0	Q6ITC6	Q737A8	Q9V9B5	MSOX_STRAW	MSOX_STRSB	SOX_HUMAN	Q61AJ9	Q63AM4	Q81PT2	Q92NL2	Q982V8	0661N9	081CN0	06н111
	08	7	~	7	~	~	~	~	7	~	~	~	7	~	~	7	~	Н	~	7	~	Н	-	-	N	~	~	N	~	~	~	7
	f Query Match Length DB	438	437	445	426	418	437	438	437	437	412	433	505	433	486	446	435	390	387	371	440	384	388	390	390	371	371	395	367	773	371	371
d	Query Match	92.1	78.4	49.1	33.5	33.5	26.1	24.9	24.8	23.7	19.3	18.4	16.9	15.3	15.0	13.9	13.7	7.6	7.3	7.2	7.2	7.2	7.2	7.0	7.0	6.9	6.9	٠		٠	6.7	6.7
	Score	2331	1982.5	1242.5	848	846.5	099	629	627	900	488.5	465	426.5	386	378.5	351	346	192	185	183	181.5	181	181	177.5	177.5	175	174	172.5	172	170.5	170	170
	Result No.	-	63	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

drosophila	oryctolagus	ralstonia s	escherichia	arthrobacte	pseudomonas	homo sapien	mus musculu		bradyrhizob		bacillus sp	oceanobacil	bacillus sp
095u69	P79371	Q8xty8	046904	P40873	Q88ge9	08n6z6	Q9d826	Q82m71	Q89m92	Q8fei5	Q6r512	QBemp0	P23342
69266	SOX RABIT	Q8XTY8	YGCN ECOLI	MSOX ARTST	Q88G <u>E</u> 9	9Z9N8Ö	SOX MOUSE	Q82M71	Q89M92	QBFEIS	Q6R5L2	QBEMPO	MSOX_BACSN
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399	390	435	423	388	382	390	390	381	410	433	331	375	387
6.7	6.7	6.7	9.9	9.9	6.5	6.4	6.3	6.3	6.3	6.2	6.1	6.1	6.1
	S	69	9.5	166	165	162.5	160	159.5	159.5	157	155	155	155
170	169.		16			_							

ALIGNMENTS

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKTOIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGC 371
                                                                                                                                                                                                         PSEQUENCE FROM N. A. Monde-9139700; DOI=10.1074/jbc.272.19.12505; M. MEDLINE-97284722; Pubmed-9139700; DOI=10.1074/jbc.272.19.12505; M. Takahashi M., Pischersrieder M., Monnier V.M.; Takahashi M., Pischersrieder M., Monnier V.M.; Takahashi M., Pischersrieder M., Monnier V.M.; Takahashi M., Pischersrieder M., Monnier V.M.; Takahashi M., Pischersrieder M., Monnier V.M.; Takahashi M., Pischersriene E. I. S. J. From Aspergillus fumigatus."; T. Biol. Chem. 272:12505-12507(1997).

REBL; WESSO; AAC49711.1; --
REBL; WESSO; AAC49711.1; --
REPL; PREOMOSO4; Picatalytic activity; IEA.

RICHEPPO; IPROMOSO4; ThiF domain.

RICHEPPO; IPROMOSO94; ThiF domain.

REML; WESUSKIE 438 AA; 48931 MW; FBC8A3E5D89D02AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 SNNKDBIEVNEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN
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                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fructosyl amine: oxygen oxidoreductase.
Appergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5085;
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99.8%; Pred. No. 9.5e-171;
iive 1; Mismatches 0;
                                438 AA
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.8*
Matches 437; — Conservative
                                PRELIMINARY;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fructosyl amine:oxygen oxidoreductase.
Aspergillus fumigatus (Sartorya fumigat).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                              Pfam; PF01266; DAO; 1. SEQUENCE 445 AA; 49364 MW; 57685EE6CA535B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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 PRELIMINARY;
                                                                                                                                        NCBI_TaxID=5085;
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VAELTRPEGFRQLAP-GVLKGNFPGWRGYHIRSNAGWAHARNALVAAAREAQRLGVRFVA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299
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                   361 GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKMNPDIAANRNWRDTLGRFGGPNRVMD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNNXDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN 131
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 431
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97175014; PubMed=9022674; Yoshida N., Sakai Y., Isogai A., Fukuya H., Yagi M., Tani Y., Kato N.; Yoshida N., Sakai Y. Isogai A., Fukuya H., Yagi M., Tani Y., Kato N.; "Primary structures of fungal fructosyl amino acid oxidases important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMD
 GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
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                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=33178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48869 MW; B838EA0AB2105E36 CRC64;
                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.4%; Score 1982.5; DB 2. Best Local Similarity 82.2%; Pred. No. 6.1e-144; Matches 360; Conservative 44; Mismatches 33;
                                                                                                                                                                     437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   for measurement of glycated proteins.";
Eur. J. Blochem. 242:499-505(1996).
EMBL; Y09020; CAA70218.1; -.
O, GO:0003824; F.catalytic activity; IEA.
Pfam; PF01266; DAO; 1.
SEQUENCE 437 AA; 48869 MW; B833BAQAB21
                                                                                                                                                                                                   Created)
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FNEVKEWTNVTQRDISKL 437
                                                            449
                                                                                 421 FHDVKEWTNVQYRDISKL 438
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                                                                                                                                                                                                                                                 Fructosyl amino acid oxidase.
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                                                            FHDVKEWTNVQYRDISKL
                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                Aspergillus terreus.
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                                                                                                                                                     74 NKD-----EIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGV-RVRPG 127
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                                                                                              366 SLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGG
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                                                                                                                                                                                                                               128 EDPNLVELTRPEQFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV
                                                                                                                                                                                                                                                                                                      188 KFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGOFLDFKNQLRPTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase.
ORNames=DBHA0A031579;
Debaryomyces hansenii CBS767.
Bukaryota, Fungi; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                       23;
Match 49.1%; Score 1242.5; DB 2; Length 445; Local Similarity 51.1%; Pred. No. 5.3e-87; les 231; Conservative 78; Mismatches 120; Indels 23;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|P78573 Aspergillus fumigatus Fructosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNRVMDFHDVKE--WINVQYRDISKLKGELEG 455
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykaten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellonz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T. "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQ----Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 426;
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Matches 181; Conservative 71; Mismatches 153; Indels
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InterPro; IPR006076; Fad_oxred.
InterPro; IPR000205; NAD_BS.
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RYGGSNEVKDLKNVKOWSN
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SEQUENCE 426 AA; 48
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Submitted (JUL-2004)
                                                                      SEQUENCE FROM N.A.
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418 AA.

PRELIMINARY;

Q6BZA7 Q6BZA7;

RESULT 5 Q6BZA7

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                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|Q92204 Aspergillus terreus Fructosyl amino acid
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tive 71; Mismatches 154;
   Created)
Last sequence update)
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                                                                                                                                                        ORFNames=DEHA0A03223g;
Debaryomyces hansenii CBS767.
25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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Matches 181; Conservative
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                                                                                                                                                                                                                                                                                   NCBI_TaxID=284592;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CBS767;
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Fructosyl amino acid oxidase.
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=162425;
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MEDLINE=97175014; PubMed=9022674;

MEDLINE=97175014; PubMed=9022674;

Woshida N., Sakai Y., Isogai A., Fukuya H., Yagi M., Tani Y., Kato N.;

"Primary structures of fungal fructosyl amino acid oxidases important for measurement of glycated proteins.";

Fur. J. Blochem. 242:499-505 [1996].

EMBL; Y09021; CAA70219.1; -.

Pfam; PF01266; DAO; 1.

SEQUENCE 437 AA; 48231 MW; E681B8702DE4A574 CRC64;
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Penicillium janthinellum (Penicillium vitale)
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Arch. Microbiol. 178:344-350(2002).
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                                                                                                                  Bukaryota; Fungi; Ascomycoča; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR16568; ARL0928.1; -InterPro; IPR0066076; Pad oxred.
InterPro; IPR000205; NAD_BS.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Name-faoA;
Emericella nidulans (Aspergillus nidulans)
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MEDLINE=22261769; PubMed=12375102;
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Matches 148; Conservative
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Similarity
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  STRAIN-NISL 9330;
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                                                                                                                                                 Matches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                  182 AQRMGVKFVTGTPQGRVVTLIF--ENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFK 239
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                                                                                                         oxidases
                                                                                                                                                                                                                                                  Gaps
                                                                      STRAIN-ATCC 18547;
MEDLINE-22937253; PubWed=14575701; DOI=10.1016/j.bbrc.2003.09.169;
Hirokawa K., Gomi K., Kajiyama N.;
"Molecular cloning and expression of novel fructosyl peptide oxidas and their application for the measurement of glycated protein.";
Blochem. Blophys. Res. Commun. 311:104-111(2003).
EMBL; AB116146; BAD00185.1; -.
GO, GO:0016491; Floxidoreductase activity; IEA.
InterPro; IPR006076; Fad_oxred.
InterPro; IPR006076; MAD_BS.
Pfam; PF01266; DAO; 1.
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Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Coniochaetales; Coniochaetaceae; Coniochaeta
                    Bukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; Eupenicillium.
NCHI_TaxID=69803;
                                                                                                                                                                                                                            Length 437;
                                                                                                                                                                                                                          24.8%; Score 627; DB 2; Length 43 34.1%; Pred. No. 1.2e-39; tive 82; Mismatches 174; Indels
                                                                                                                                                                                                       437 AA; 48187 MW; A79159C804B63848 CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Pructosyl peptide oxidase.
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            Supenicillium terrenum.
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                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               153;
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Best Local ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22937253; PubMed=14575701; DOI=10.1016/j.bbrc.2003.09.169; Hirokawa K., Gomi K., Kajiyama N.; Morellar cloning and expression of novel fructosyl peptide oxidases and choile application for the measurement of glycated protein."; Biochem. Biophys. Res. Commun. 311:104-111(2003).

EMBL; AB11647; BAD00186.1; -. InterPro; IPR006076; Fad oxred.

InterPro; IPR000205; NAD—BS.
Pfam; PP01266; DAO; 1.

SEQUENCE 437 AA; 48634 MW; 5702BCFFDIC2D979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 IEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL-VELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 R---PEQFRKLAPEGVLQGD-FPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTG
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                                                                                                                                                                                                                                                                                                                            23.7%; Score 600; DB 2; Length 437; 32.7%; Pred. No. 1.4e-37; Live 86; Mismatches 162; Indels
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Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 AA
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- DIAANRNWR 417
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NCBI_TaxID=4896;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                Schizosaccharomyces pombe (Fission yeast).
                                                         Schizosaccharomyces.
                                                                                              SEQUENCE FROM N.A.
 Name=SPAC139.04c;
                                                                     NCBI_TaxID=4896;
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        Mooney P., Moule S., Mungali K., Murphy L., Niblett D., Odell C., Olver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Skelton J., Studeres R., Steuches E., Stelton J., Studenes R., Skelton J., Stummonds M., Squares R., Steuches K., Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., Weltjens I., Volckaer G., Aert R., Robben J., Gyrmonprez B., Weltjens I., Vanstreels E., Rager M., Schafer M., Muller-dar S., Hulbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 PGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMMSIPFEKTQI----PKEAETRVRALLKETM-PQLADRPFSFARICWCADTANREFLID 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 KVESVPPKKPLVSPILPKEAELDLRRNLQRTYGEEISQRPFYKTRICYYTDTADAEFVFD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 YHPDYENLFVCTGGSGHGFKFFPILGKYSIGCMPRELEEPLIKKWRWKKENLEFAALDHS 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSA-----CSQEGLDRLGVRVR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL-DFKNQLRP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVSFISG-PEGTVEELITEENVVKGVRTTTG-AYMAEKLIFATGAWTASLLPNDHTRFLA 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 TAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADG
                                                                                                                                                                                                                                                                                                                                                                                                                               41; Gaps
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.
                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 488.5; DB 2; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.8e-29;
78; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                     46319 MW; BD36B86075D3F4EF CRC64;
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InterPro; IPR000205; NAD_BS.
                                                                                                                                                                                                                                                                    Nature 415:871-880(2002).
EMBL; AL022071; CAA17815.1; -.
PIR; T40295; T40295.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01266; DAO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Q9UTM9
ID Q9UTM
AC Q9UTM
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DT 01-MA
DT 01-MA
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Created) Last sequence update) Last annotation update)

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01-MAY-2000 (TrEMBLre 01-MAY-2000 (TrEMBLre 01-MAR-2004 (TrEMBLre SPAC139.04c protein.

PRELIMINARY;

Q9UTM9; Q9UTM9

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Mood V., Gwilliam R., Rajandraem M.A., Lyne R., Stewart A.,
Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Byooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Gentles S., Gonbe A., Hamlin N., Harris D., Hidalgo J., Hodgen G.,
An James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Annoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Annoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Annoney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,
Anterford K., Rutter S., Saunders D., Sequres S.,
Skelton J., Simmonds M., Squares R., Squares S.,
Skelton J., Simmonds M., Squares R., Squares S.,
Anterfork K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
Antipert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Antibert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
Antibert H., Barzym K., Langer I., Sachez M., Garzon A., Thode G.,
Antes M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
Antes M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
Antes M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
Anter G., Lowe T., McCombie W., Paulsen I., Potashkin J.,
Cerutti L., Lowe T., McCombie W., Paulsen I., Potashkin J.,
The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNALVAAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 KLLGDSALINLSSSEEIRKKYPSLFSNSPLRSDMOA----VVNEHAGYANSAASLKLLEL 165
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EBBL; ALI32667; CABS9618.1; -.
PIR; T37605; T377605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 DEIEVNEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGE----
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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
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18.4%; Score 465; DB 2; Length 43
Best Local Similarity 30.1%; Pred. No. 3.3e-27;
Matches 130; Conservative 80; Mismatches 174; Indels
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SEQUENCE 433 AA; 48973 MW; 170081BB3D48B1BE CRC64;
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InterPro; IPR0006076; Fad_oxred.
InterPro; IPR000583; GATase_2.
Pfam; PF01266; DAO; 1.
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SSGOYSNNKDEIEVNEILAEEAFNGWK-----NDPLFKPYYHDTGLLMSACSOEG-LDRL 120
                      250 TGARLSDGRVLSADLVMVSAGAWTGRLVDLTGQALATGQVLGYIDLTPEEEAQLAHMPVI 309
                                                                                                                                                                                                                                                                                                                                                                                               -----QIPKEAETRVRALLKE--TMPQLADRPFSFARICWCADTANREFLIDRHPQYH 365
                                                                                                                                                                                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerlch J.M., Beyne E., Blaykasten C.,
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A Kerrest A., Kosaul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
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Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                             198 --GSSGSW-GYI-NGLSGWANAGASMAMLYKRVRAEGRINFVA----GEVTNLEVSGNTV
                                                                                                                                                                                                                                                                                                                                        139 GTPVAPGTSVIDKSKLTGMDYARFSWANVLSLASSDPELAARIKECPNTDAIKAALGTG-
                                                                                                                                                                                                                                    209 KGAVTGDGKIWRAERTFLCAGASAGQFLDFKNOLRPTAWTLVHIALKPEBRALYKNIPVI
                                                                                                                                                                                                                                                                                                               269 FNIERGFFFEPDEERGEIKICDEHPGYTNWVQSADGTMMSIP----FEKT-----
                                                                               ----EDPNLV----ELTRPEOFRKLAPEGV
                                                                                                                                                        150 LOGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG-VKFVTGTPQGRVVTLIFENNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp[QUTM9 Schizosaccharomyces pombe Putative fructosyl
amino acid oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 SLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=KULA0F02860g;
Kluyveronyces lactis NRRL Y-1140.
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6CLIO;
25-OCT-2004 (TrEMBLrel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, CR382126; CAG97917.1; -.
InterPro; IPR006076; Fad oxred.
InterPro; IPR000205; NAD_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome evolution in yeasts.";
Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01266; DAO; 1.
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                                                                               GVRVRPG-
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Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
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Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
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Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                    YEYVCHVETDYDENSKYVSIPHSGPSKSSLPKYAIIQMRRFLDTFLDTLADKSLINTKMC 344
                  PGYTNMVQS---ADGTWMSIPF---EKTQIPKEAETRVRALLKETMPQLADRPFSFARIC 346
                                                                                           347 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 406
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29.2%; Pred. No. 3.7e-24;
ive 56; Mismatches 169; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-GCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Related to fructosyl amino acid oxidase)
Name=NCU04771.1; Synonyms=B15B10.150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   German Neurospora genome project;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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EMBL; BX897677; CAE85581.1; -.
InterPro; IPR006076; Fad_oxred.
Pfam; PF01266; DAO; 1.
Hypotherical protein.
SEQUENCE 502 AA; 52930 MW; 39748F9E553D4FDE CRC64;
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RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
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RI "Genome evolution in yeasts.";
L Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                133 VELTRPEQFRK-----LAPEGVLQGDFPGWKGYFARS------GAGWAHARNALVA 177
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|P78573 Aspergillus fumigatus Fructosyl amine: oxygen
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Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                       82;
                           DB 2; Length 433;
                                                                       67; Mismatches 167; Indels
                        15.3%; Score 386; DB 2 28.3%; Pred. No. 4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 KVISSGOYSNNKDEIEVNEILAEEAFNGWKN------DPLFKPYYHDTGL-LMSAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 GWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVT-LIFENNDVKGAVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYP------VPSAISAGNDVN
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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25-OCT-2004 (TIEMBLrel. 28, Last annotation update)
Similar to tr|043029 Schizosaccharomyces pombe Putative fructosylamino acid oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
NCBI_TaxID=284592;
                                                                                                                                                                                                                                                                                                                                                                                 75;
                                                                                                                                                                                                                                                                                                                        Length 486;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
to the EMBL/GenBank/DDBJ databases.
                                                                                 InterPro; IRR006076; Fad oxred.
InterPro; IRR006076; Fad oxred.
InterPro; IRR000408; Reg chr condens.
InterPro; IRR000594; Thif domain.
Pfam; PF01266; DAO; I.
PROSITE; PS00626; RCCI 2; UNKNOWN 1.
SEQUENCE 486 AA; 55220 MW; 5861D01F87F8C830 CRC64;
                                                                                                                                                                                                                                                                                                                     / Match 15.0%; Score 378.5; DB 2; Local Similarity 28.9%; Pred. No. 1.7e-20; nes 129; Conservative 60; Mismatches 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 ACGGSGHAFKMLPVLGQFLVDKIEGR 433
                                 L, CR382138; CAG88679.1; -. GO:0003824; F:catalytic activity;
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Debaryomyces hansenii CBS767.
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223 AAGAWSCKLVNLDNISKSSAIEVVWFKVTPSMEKEWKQMSITTTNLSTGINIFPP--YNGE 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 NNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGL------LMSACSQEGL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 DRLGVRVRPGEDPNLVELTRPEQ-FRKL---APEGVLQGDFPG---W-KGYFARSGAGWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 HARNAL -- - VAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | :: | | : : | | : : | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : : | | | : : | | | : : | | : : | | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Pairhead C., Ferry-Dumazet H., Groppi A., Handrraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Kosull R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B., Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wickner P., Souciet J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 351; DB 2; Length 446; 26.8%; Pred. No. 2e-18; tive 74; Mismatches 186; Indels 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000205; NAD_BS.
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Matches 126; Conservative
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Search completed: May 27, 2005, 13:47:31 Job time: 104.659 secs

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May 27, 2005, 13:28:05 ; Search time 179.139 Seconds (without alignments) 1019.048 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           protein search, using sw model
                                                                                                           OM protein -
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Run on:

US-10-622-893A-5 2530 1 MGGSGDDDDALALAVTKSSSL.....LEGLPIPNPLLRTGHHHHHH 472 Title: Perfect score:

Scoring table: Sequence:

2105692 segs, 386760381 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* A_Geneseq_16Dec04:* 1: geneseqp1980s:* geneseqp20048:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	1982.5	78.4	437	~	AAW39253	
8	1982.5	78.4	437	~	AAY29100	Aay29100 A. terreu
ų	1977.5	78.2	437	~	AAW37141	Aaw37141 Aspergill
4	1158.5	45.8	440	7	AAW69251	Aaw69251 Fructosyl
Ŋ	1158.5	45.8	440	ß	ABG30782	Abg30782 Fusarium
y	1152.5	45.6	440	S	ABG30784	Abg30784 Fusarium
7	1151.5	45.5	440	ß	ABG30785	Abg30785 Fusarium
80	1150.5	45.5	440	ß	ABG30783	Abg30783 Fusarium
6	1115.5	44.1	444	œ	ADM78789	Adm78789 Fusarium
10	837.5	33.1	427	æ	ADS15771	Ads15771 Fructosyl
11	661	26.1	432	7	ADE81213	Ade81213 Orf20, SE
12	099	26.1	437	~	AAW24134	Aaw24134 Fructosyl
13	099	26.1	437	~	AAW97386	Aaw97386 A fructos
14	099	26.1	437	7	AAW97387	Aaw97387 A fructos
15	627	24.8	437	9	ABR41990	Abr41990 Eupenicil
16	900	23.7	437	9	ABR41989	Abr41989 Coniochae
17	437.5	17.3	439	Ŋ	ABB78358	Abb78358 Amino aci
18	416.5	16.5	473	6 0	ADM78787	Adm78787 Fusarium
19	330.5	13.1	109	~	AAW69252	Aaw69252 Fructosyl
20	198	7.8	411	7	ADC59522	Adc59522 Arthrobac
21	192	7.6	390	ч	AAP94663	Aap94663 New sarco
22	192	7.6	390	7	AAW07397	Aaw07397 Bacillus
23	184	7.3	389	~	AAR23780	
24	181.5	7.2	440	4	ABB59342	Abb59342 Drosophil
25	177.5	7.0	390	4	ABB08949	Abb08949 Human ser

Aam40278 Human pol	Aab94212 Human pro	Aam42064 Human pol	Aaw71462 A modifie	Aar38078 Sarcosine	Aar52658 Arthrobac	Aar79150 Arthrobac	Aar76735 N-methyl	Aaw25148 Arthrobac	Aaw71461 A modifie	Aaw53155 Arthrobac	Aab99724 Arthrobac	Ado23559 Arthrobac	Aaw25150 Modified	Aaw25151 Modified	Aaw53164 Arthrobac	Aag98942 E. coli g	Abul4777 Protein e	Aaw53163 Arthrobac	Abu40301 Protein e
AAM40278	AAB94212	AAM42064	AAW71462	AAR38078	AAR52658	AAR79150	AAR76735	AAW25148	AAW71461	AAW53155	AAB99724	AD023559	AAW25150	AAW25151	AAW53164	AAG98942	ABU14777	AAW53163	ABU40301
4	4	4	~	7	~	~	7	~	~	7	4	80	~	~	~	4	9	~	ø
390	390	400	389	387	389	389	389	389	389	389	389	389	389	389	389	433	433	389	385
7.0	7.0	7.0	6.9	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	6.5
		'n.	171	169	169	169	169	169	169	169	169	169	168	168	168	168	168	167	165
177.5	177.	177.5																	

ALIGNMENTS

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This sequence represents a novel recombinant fructosylamino acid oxidase (FAOD-L) produced from eukaryotic cells integrated with an RT-PCR product encoding FAOD-L derived from Aspergillus terreus GPI (FERM P-15664). FAOD-L can be used for the analysis of "Amadori" compounds
                                                                                                                                                                                                                                                                                                                                                              Aspergillus terreus recombinant fructosyl:amino acid oxidase - used for analysis of "Amadori" compound(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Score 1982.5; DB 2; Length 437; 82.2%; Pred. No. 9.5e-188; ive 44; Mismatches 33; Indels 1;
                                                                                                                                  Fructosylamino acid oxidase; FAOD-L; Amadori compound.
                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 23-26; 18pp; Japanese.
                         AAW39253 standard; protein; 437 AA.
                                                                                                                                                                                                                                                                                              (KYOT-) KYOTO DAIICHI KAGAKU KK.
                                                                                                                                                                                                                                           96JP-00194557.
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                                                                             14-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                     A. terreus FAOD-L protein.
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N-PSDB; AAV09626.
                                                                                                                                                          Aspergillus terreus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 437 AA;
                                                                                                                                                                                    JP10033180-A.
                                                                                                                                                                                                                                                                     24-JUL-1996;
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Best Local Simil
Matches 360; C
                                                                                                                                                                                                                10-FEB-1998.
                                                   AAW39253;
RESULT 1
           AAW39253
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SNNKDBIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN 131

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359
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                                                                                                                                                                                                               311
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                                                                                                                                                                                                                                                                  371
                                                                                                                                                                                                                                                                                                                   431
                                                     SNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN 131
 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises an Aspergillus terreus fructosyl amino acid oxidase (FAAO), designated FAOD-L, that shows higher FAAO activity on fructosyl lysine than on fructosyl lits amino acid sequence was deduced from a cDNA clone (see AAV00732) obtained from an A. terreus GP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant fructosyl amino acid oxidase - useful in assays for amadori compounds, e.g. in diabetes diagnosis or food analysis.
                                                                                                                                                                                                            GTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVH
                                                                                                                                                                                                                                                                  EKTOI PKEAETRVRALLKETMPOLADRPFSFARI CWCADTANREFLIDRHPQYHSLVLGC
                                                                                                                                                                                                                                                                                                                     GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMD
12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fructosyl amino acid oxidase; FAOD-L; amadori compound; assay; food analysis; diabetes; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus terreus fructosyl amino acid oxidase.
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                                                                                                                                                                                                                                                                                                                                                                         FHDVKEWTNVQYRDISKL 449
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FNEVKEWTNVTQRDISKL
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                                                                                                         LVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVT
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S-transferase; GST; Amadori compound.
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Best Local Similarity 82.2
Matches 360; Conservative
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glutathione S-transf
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Amadori compounds.
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cDNA library. The invention provides recombinant FAAO, DNA encoding the AFAO, an expression vector containing the DNA, a transformant transformed by the vector, and a method of preparing recombinant FAAO by culturing the transformant. The FAAO can be used in assays for, e.g. determination of amadori compounds such as glycated blood proteins, diagnosis and monitoring of diabetes or quality control of foods. (Updated on 17-OCT-2003 to standardise OS field)
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N-PSDB; AAV44893.
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                                                                Sequence 437 AA;
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                                                                                                              by the microbe of oxidase with high
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TADSKGDDEDSIWKALSYAAAQGWLHDPVFQPFCHNTGSVVAGSTPKSIKQL-VEDEIGD
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                                                                                                                                                                                                                                                                                                                                        11 ALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVIS--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-PNLVELTRPEOFRKLAPEGVLOGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHS
microorganism - used for producing fructosylamine
                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                          / Match 45.8%; Score 1158.5; DB 2; Length 440; Local Similarity 51.1%; Pred. No. 9.1e-106; nes 224; Conservative 75; Mismatches 132; Indels 7;
                                                                                                         This sequence is the fructosylamine oxidase produced by the invention. The microbe can produce fructosylamine o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by ATG"
Misc-difference 396
                                                                 Claim 1; Page 11-13; 15pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRVMDF -- HDVKEWTNVQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein;
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                         efficiently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxysporum.
                                                                                                                                                                                                       Sequence 440 AA;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-599854/64.
                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium oxysporum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK90477
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                  ABG30784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kouzuma
                                                                                                                                                  ABG30784
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a (4-(2-hydroxychyl)-1-piperazinyl group. The invention also relates to compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and brommoresel purple for evaluation of glycation of proportion of albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease
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                                                                                                                                                                                                                                                                                                                Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 GQYSNNKDEIEVNEILABEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 LVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-PNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 MSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 1158.5; DB 5; Length
51.1%; Pred. No. 9.1e-106;
.ive 75; Mismatches 132; Indels
                                                                                                                                                                                                                                 Sumitani J, Imamura
/note= "Encoded by TTC"
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 63-65; 82pp; Japanese
                                                                                                                                                                                                                                   Kouzuma T, Yoshioka I, Arai M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the scope of the invention
                                                                                                                               31-JAN-2001; 2001JP-00022953
16-FEB-2001; 2001JP-00039796
                                                                                                30-JAN-2002; 2002WO-JP000721
                                                                                                                                                                 08-AUG-2001; 2001JP-00240002
                                                                                                                                                                                                  (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224; Conservative
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                                                                                                                                                                                                                                                                 WPI; 2002-599854/64.
N-PSDB; ABK90475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 440 AA;
                                                                   08-AUG-2002
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The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a 4-(2-hydroxyethyl)-1-piperazinyl group. The invention also relates to determining glycoalbumin and a protein-denaturing agent and/or a compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation proportion of albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease
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360 LVIASGDCGTGYKHITSIGKFISDCMEGTLEERFAKYWRWRPEKFTEFWGKDPLDRFGAD 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoamino acid; glycoprotein; deoxycholic acid; deoxycholic amide; cholic acid amide octyl glucoside; quaternary ammonium salt; quaternary ammonium salt; acidinic surfactant; concanavalin h; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes; ascorbic acid; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG30784 standard; protein; 440
                                                                                                                                                427 NRVMDF--HDVKEWTNVQ 442
                                                                                                                                                                                                            420 DKIMDLPKSDVEGWINIK 437
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08-AUG-2001; 2001JP-00240002.
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NRVMDF--HDVKEWTNVQ 442
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                         30-JAN-2002;
                                                                                                                                                                            Kouzuma T,
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                                                                                                                                                                                                                                                                                                                            D-PNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGP 426
                                                                                                                                                                                                              9
acting on glycoamino acids. This sequence represents a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholic acid amide octyl glucoside; quaternary ammonium salt; quaternary ammonium salt cationic surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes; ascorbic acid; mutant; mutein.
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                                                                                                                                       7;
                                                                                                  Length 440;
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                                                                                                                                       Indels
                                                                                                  DB 5;
                                                                                            45.6%; Score 1152.5; DB 5; 50.9%; Pred. No. 3.6e-105; iive 75; Mismatches 133;
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DKIMDLPKSDVEGWTNIK 437
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                                                                                                                 Local Similarity
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                                                          Sequence 440 AA;
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The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid anide octyl glucoside, queternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a (2-hydroxyethyl)-1-piperazinyl group. The invention also relates to compositions for assaying albumin contanting the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation cabuunin into glycoalbumin with respect to the other albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease acting on glycoamino acids. This sequence represents a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including
                                                                                                                                                                                                                                                                                                                                                                                                    s,
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                                                                                             31-JAN-2001; 2001JP-00022953
16-FEB-2001; 2001JP-00039796
08-AUG-2001; 2001JP-00240002
2002WO-JP000721
                                                                                                                                                                                                                                                                                                                                                                                                    Yoshioka I,
                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI
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128 61 TADSKGDDEDSIWKALSYAAAQGWLHDPVFQPFCHNTGSVVAGSTPKSIKQL-VEDEIGD 119 187 179 247 9 1 ASTLTKOSOILIVGGGTWGCSTALHLARRGYTWVTVLDVNRIPSPISAGHDVNKLAGRLS GQYSNNKDEI EVNEI LAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGE KFVTGTPQGRVVTL1FENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAW ALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVIS--S D-PNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV Gaps 7; Length 440; Indels DB 5; 45.5%; Score 1151.5; DB 5; 50.9%; Pred. No. 4.5e-105; iive 75; Mismatches 133; Query Match
Best Local Similarity 50.9%

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68

359 239 TLVHIALKPEERALYKNI PVI FNI ERGFFFEPDEERGEI KI CDEHPGYTNMVQSADGTM- 306 MSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHS 366 LVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGP 426 300 QSIPFAKHQVPTEAERRAKKQFLKDIMPQLADRPLVHARICWCADTQDRAFLITYHPRHPS

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7;

Length 440; Indels 128 119

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187 179 247 239

306

299 366 359 426 419

RESULT

420

05-NOV-2002

ABG30783

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fructosylamine oxidase; fructosyllysine; fructosylvaline;
Amadori compound; medical examination; diagnosis; serum glucose level;
food inspection; enzyme.
                                                                                                                                                                                             240 TLGHIQITPEETKLYKNLPPLFNINQGFFMEPDEDLHQLKMCDEHPGYCNWVEKPGSKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 OSIPFAKHQVPTEAERRAKQFLKDIMPQLADRPLVHARICWCADTQDRMFLITYHPRHPS
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                                                                                                             69 GQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGE
                                                                                                                                                                                                                                                          D-PNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGV
                                                                                                                                                                                                                                                                                  248 TLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 LVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGP
                                                                                                                                                                                                                                                                                                                                                 188 KFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusarium proliferatum fructosylamine oxidase Q2 protein sequence
  DB 5;
45.5%; Score 1150.5; DB 5
50.9%; Pred. No. 5.7e-105;
ive 75; Mismatches 133;
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                                            223; Conservative
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                        Similarity
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    Query Match
                        Best Local
Matches 22
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                                                                                                                                                                                                                                                                                Glycoamino acid; glycoprotein; deoxycholic acid; deoxycholic amide; cholic acid amide octyl glucoside; quaternary ammonium salt; quaternary ammonium salt cationic surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxychyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Wild-type Lys substituted by Trp. Encoded by
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246
                                                                                                             ABG30783 standard; protein; 440 AA.
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    DKIMDLPKSDVEGWTNIK 437
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16-FEB-2001; 2001JP-00039796
08-AUG-2001; 2001JP-00240002
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                                                                                                                                                                                                (first entry)
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N-PSDB; ABK90476.
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08-AUG-2002

Synthetic.

Fusarium proliferatum-originated fructosylamine oxidase useful in measurement of Amadori compound and particularly applicable in medical examination including diagnosis and management of diabetes.

Sequence 440 AA;

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ADE81213 standard; protein; 432
               30-SEP-2004
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ID ADE8
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                    The invention relates to a novel fructosylamine oxidase isolated from Fusarium proliferatum. The enzyme has the following physiochemical characteristics: (a) activity against fructosylylshine equivalent to or higher than that against fructosylvaline; (b) optimum pH for enzyme activity of 7.5; (c) enzyme stability optimally at 30-40 deg C; and (d) a molecular weight of about 39 kDa as measured by SBS-PAGB and about 39.4 characterized by: (i) activity against fructosylvaline and no detectable activity against fructosylvaline and no detectable activity against fructosylvaline and no detectable activity against fructosylvaline and no detectable activity against fructosylvaline and sour SB kDa by gel filtration. The oxidases are useful in the measurement of Amadori compounds and particularly applicable in medical examination including for treatment and prevention of diabetes by controlling serum glucose level for treatment and prevention of complications, and in food inspection. This sequence represents the fructosylamine oxidase designated Q2.
                                                                                                                                                                                                                                                                                                                                                                  SKGDDEDSIWKALTYAAAQGWLHDPIFQPFCHNTGAVWAGSTPKSIKQL-VEDEIGDDID 126
                                                                                                                                                                                                                                                                                                                                                                                                                 QYTPLNTAEDFRRTMPERILIGDFLGWKGFYKPRGSGWVHARKAMKAAFESQRLGVKFI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 NK--DEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGED-P 130
                                                                                                                                                                                                                                                                                                                                                                                                     NLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTM-MSI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASGDCGTGYKHITSIGKFISDCWEGTLEERFAKFWRWRPEKFTEFWGKDPLDRFGADDKI 426
                                                                                                                                                                                                                                                                                                                   14 VTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fructosylamine oxidase; enzyme; fructosylamine; fructosyl valine
                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                        Length 444;
                                                                                                                                                                                                                                                                             71; Mismatches 138; Indels
                                                                                                                                                                                                                                                       44.1%; Score 1115.5; DB 8; 50.3%; Pred. No. 1.7e-101;
 NO 6; 50pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fructosylamine oxidase, SEQ ID 1.
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MDLPKSDAEGWTDIQ
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                 Local Similarity
les 219; Conserv
                                                                                                                                                                                                                               Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004083419-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 VRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to fructosylamine oxidase protein (1; ADS15771) and its coding sequence (II; ADS15772) from Pichia sp. preferably Pichia sp. N1-1 strain. (I) is useful for spectroscopic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine compounds. (I) is also useful for analyzing fructosyl valine by spectroscopy, which involves degrading HDAIC, fructosamine or glycoalbumin in a sample using (I) to produce fructosyl valine or fructosylamine, respectively. (I) is also useful for carrying out electrochemical analysis of HDAIC, fructosamine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                            Novel fructosylamine oxidase protein, useful for spectroscopic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine and fructosyl valine compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SIPLYRMEIPLESALEIRQYLKETMPQFADRPFTKTRICWCTDSPDMQLILCTHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 NKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQ------EGLDRLGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 RMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 PTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHSLVLGCGASGRGFKYLPSIG----NLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 SLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKV----ISSGQYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.1%; Score 837.5; DB 8; Length 427; ilarity 39.3%; Pred. No. 7.5e-74; Conservative 85; Mismatches 141; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LG--RFGGPNRVMDFHDVKEWTNVQYRDISKLK 450
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RGOVRWGGRYRVADLNEIEEWVSVENPTPHKLE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1; 51pp; Japanese.
17-MAR-2004; 2004WO-JP003587
                                                           17-MAR-2003; 2003JP-00116348
                                                                                                                                                                                                                                     2004-709934/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                     N-PSDB; ADS15772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 427 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 QLTAKGHSVAHIQLTPSETKHYASMPIMDNLELGYFFPPQED-GIFKMA--HSQFITNVQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 TTKSGITTSVPHTFVQAPTDGLPLEIEAQMRRNLRRVLPELADRPFCYTRLCWDADTADR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 QEKGVKYISGKTKGDVQELILDDITGECKGVVTADGTRHEADVVILAAGAWTPSLLDVKG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFFEPDEERGEIKICDEHPGY-TNMV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEIEVNE----ILAEEAFNGWKNDPLFKPYYHDTGLLMSAC------SQEGLDRLGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 QSADGTWMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARICWCADTANR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DPEIVSQW 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DYNEPLYARLGIESIEAWRSWSLFRGLYHVPGWILSAANLSRPFVEGSIETCKRLGV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                      The present invention relates to a DNA sequence (I, ADE81173), which is associated with ML-226B synthesis. (I) is useful for improving ML-236B production in a HMG-COA reducing-enzyme-inhibitor ML-236B producing microbe. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        16 KSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                    RVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRMGVKFVTGTPQGRVVTLIFEN--NDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKN
                                                                                                                                                                                                                                                     useful for improving
                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                                                               26.1%; Score 661; DB 7; Length 432; 35.7%; Pred. No. 2.8e-56; Live 68; Mismatches 168; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H: | | : | | | | | | | | | | | | | HELVIPHPAHKSLFLATGGSAHGFKFLPVVGKYVADLLEGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWR----DILGREGGPNRVMDFHDVKEWINVQYRDIS 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA associated with synthesis of ML-236B,
                                                                                                                                                                                                                                                               microbe.
                                                                                                                                                                                                                                                                                    Example 8; SEQ ID NO 41; 142pp; Japanese.
                                                                       enzyme; Orf20
                                                                                                                                                                                                                                                               236B production in ML-236B producing
                                                                                                                                                       15-OCT-2001; 2001JP-00316578
                                                                                                                                                                             15-OCT-2001; 2001JP-00316578
                             (first entry)
                                                                       ML-236B; HMG-CoA reducing
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 35.7 les 163; Conservative
                                                                                                                                                                                                 (SANY ) SANKYO CO LID
                                                                                          Penicillium citrinum
                                                                                                                                                                                                                      2003-817677/77
                                                                                                                                                                                                                                 N-PSDB; ADE81212
                                                                                                                                                                                                                                                                                                                                                           Sequence 432 AA;
                                                                                                               JP2003116567-A.
                             29-JAN-2004
                                                                                                                                    22-APR-2003
                                                 Orf20, SEQ
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         ADE81213;
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and related
body fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NM-----VQSADGTWMSIPFEKTO----IPKEAETRVRALLKETMPQLADRPFSFARIC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GLEKTINIWLESEDDILAKAPH-FTREQIKGWKGLFCGDG-GWLAAAKAINAIGTFLKSQG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 RNGPDLQ----LSLEALDMWKNDPLFKPFFHNVGMLDCSSSQEGIASLRRKHQDLIDANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 KSSSLLIV-GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNKDEIBVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSOEGLDRLGVRVRPGEDPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VELTRPEOFRKIAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT
                                                                                                                                                                                                              Fructosyl amino acid oxidase; FAOD-P; enzyme; amadori compound; alpha-ketoaldehyde amine derivative; amadori detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fructosyl amino acid oxidase which oxidises amadori compounds DNA - used for detection of amadori compounds in foods and in such as blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 437;
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AAW24134 standard; protein; 437
                                                                                                                                                            Fructosyl amino acid oxidase
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Best Local Similarity 33.6%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakai Y, Tani Y,
                                                                                                                                                                                                                                                                                               Penicillium janthinellum
                                                                                                       (first
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                                                     AAW24134;
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                                                                                                    348 WCIDTADANLLICEHPKWKAPILATGDSGHSPKVLPNIGKHVVELIEGRLPQDLAGAWRW 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNGPDLQ----LSLEALDMWKNDPLFKPFFHNVGMLDCSSSQEGIASLRRKHQDLIDANI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present DNA sequence represents a fructosylamino acid oxidase (PAOD-P). The present sequence is derived from Penicillium janthinellum S-3413, and was used to construct a synthetic sequence using primers AAX15951-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding fructosylamino acid oxidase - synthetically designed and
                                               DLEDQCVSKAWVFAHIQLTPQESAQYKDVPVVYDGDYGFFFEPN-EHGVIKVCDEFPGFS
                            297 NM-----VQSADGTMMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARIC
                                                                                   347 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLEKTNIWLESEDDILAKAPH-FTREQIKGWKGLFCGDG-GWLAAAKAINAIGTFLKSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSSSLLIV-GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYS
                                                                                                                                                                                                                                                                                                                                                                  Fructosylamino acid oxidase; FAOD-P; Penicillium janthinellum S-3413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                                                                                                                              407 NP------DIAANRNWRDTLGRFGGPNRVMDFHDVK 436
                                                                                                                                                                         RPGGDALKSKRSAPAKDLAEMPGWK--------HDAK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.1%; Score 660; DB 2; Length 43 Best Local Similarity 33.6%; Pred. No. 3.5e-56; Matches 156; Conservative 75; Mismatches 157; Indels
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N-PSDB; AAX15950.
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                                                                                                                                                                                                                                                                               AAW97387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a fructosylamino acid oxidase (FAOD-P), and is encoded by a synthetic sequence. The the wild type FAOD-P sequence is derived from Penicillium janthinellum S-3413. The synthetic sequence was constructed using primers AAX15951-6006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 NNKDEIEVNEILAERAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLEKTINIWLESEDDILAKAPH-FTREQIKGWKGLFCGDG-GWLAAAKAINAIGTFLKSQG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKFVTGT------PQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT 296
RFKLHQPYGATSPKLISVPRSHAKHPTDTYPDSSEETIRKAIARFMPRFKDKELFNRSMC 347
                           WCADTANREPLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 406
                                             coding fructosylamino acid oxidase - synthetically designed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 KSSSLLIV-GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVISSGQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fructosylamino acid oxidase; FAOD-P; Penicillium janthinellum S-3413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 437;
                                                                                   NP-----DIAANRNWRDTLGRFGGPNRVMDFHDVK 436
                                                                                                                 -----HDAK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 660; DB 2; Length 43:
ilarity 33.6%; Pred. No. 3.5e-56;
Conservative 75; Mismatches 157; Indels
                                                                                                                RPGGDALKSKRSAPAKDLAEMPGWK-
                                                                                                                                                                                       AAW97386 standard; protein; 437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 8-10; 21pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOT-) KYOTO DAIICHI KAGAKU KK
                                                                                                                                                                                                                                                                             A fructosylamino acid oxidase,
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Penicillium janthinellum
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                                                                                                                                                                       296
                                 NM-----VQSADGTMMSIPFEKTQ----IPKEAETRVRALLKETMPQLADRPFSFARIC 346
                                                                                                                                                                                                                                                       347 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 406
                                                                                                                                                                                                                                                                                            New fructosyl peptide oxidases useful as enzymes for clinical diagnosis.
DFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYT
                                                                                                                                                                                                                                                                                                                                                                                       407 NP------DIAANRNWRDTLGRFGGPNRVMDFHDVK 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fructosyl peptide oxidase; enzyme; diabetes; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 RPGGDALKSKRSAPAKDLAEMPGWK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 31-34; 59pp; English.
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12-DEC-2001; 2001JP-00378151.
06-AUG-2002; 2002JP-00228727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIKK ) KIKKOMAN CORP
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Length 437;

24.8%; Score 627; DB 6; Length 437 34.1%; Pred. No. 6.8e-53; .ive 82; Mismatches 174; Indels

Query Match
Best Local Similarity 34.1:
Matches 153; Conservative

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126
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                                                                                                                                                                                                                                                                            173 LQDKGVKFGFG-GAĞTFQQPLFAADGKTCIGLETTDĞTKYFADKVVLAAGAWSPTLVDLE 231
                                                                                                                                                                                                                                                                                                                                                                                                                     ----VQSADGTWMSIPFEKTQIPKE----AETRVRALLKETMPQLADRPFSFARICWCA 349
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67
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12 LAVTKSSSLLIV--GAGTWGTSTALHLARRGYT--NVTVLDPYPVPSAISAGNDVNKVIS
                                                                                68 SGQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRP-
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                     410 IAANRNWRDTLGRFGGPNRVMDFHDVKEW 438
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Job time : 181.139 secs
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Sequence 5, Appli
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Sequence 412, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-213-888-25
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US-09-466-647A-118
US-08-391-339-18
US-09-266-437-18
US-09-266-965-135-18
US-09-543-681A-6873
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US-09-328-331-588-27
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US-09-949-016-10219

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US-09-489-039A-12890

US-09-489-039A-12890

US-09-331-339-18

US-09-302-540-986

US-09-549-681A-6873

US-09-543-681A-6873

US-09-331-568A-274566
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence 5, Appli
Sequence 9, Appli
Sequence 1136, Ap
Sequence 81, Appl
Sequence 14, Appl
Sequence 2, Appli
Sequence 7529, Ap
Sequence 5943, Ap
Sequence 18996, A
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                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: 5948659
GENERAL INFORMATION: APPLICANT: KATO, NOBUO
APPLICANT: SAKAI, YASUYOSHI
APPLICANT: TANI, YOSHTKI
APPLICANT: TANI, YOSHTKI
APPLICANT: PUKUYA, HIROSHI
TITLE OF INVENTION: BECOMBINANT FRUCTOSYL AMINO ACID
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                              US-09-543-681A-7036
US-09-450-072-81
US-09-351-348-81
US-08-804-227C-14
US-08-804-227C-8
US-09-804-198-2
US-09-489-039A-7529
US-09-543-681A-5943
US-09-552-991A-18996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,059
                                                                                                                                                                                                                                  US-09-684-405-12
US-09-602-787A-80
US-09-252-991A-20386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILING APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/899,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, WARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 0020-4253P
TELEPHOME: (703) 205-8000
TELEPHOME: (703) 205-8000
TELEPHOME: (703) 205-8000
TELEPHOME: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDENNESS: not relevant
                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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Best Local Similarity 82.2
Matches 360; Conservative
                                MOLECULE TYPE: protein
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ZIP: 22040-0747
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 120; Conserv
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                                                                   SNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPN 131
                                                                                   180 GSPQGRVITLIFENNDVKGAVTADGKIWRAEQTILCAGAAAGGFLDFKDQLRFTAWTLVH 239
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                                                                                                                                                                                                                                                                               240 IQLKPBERAQYKNMPVVFNIEKGFFFEDDEERGEIKICDEHPGYTNMTTGADGRVRSIPF 299
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                                                                                                                                                                                                                                                                                                                                                                                              GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMD 431
                                                                                                                                  LVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRMGVKFVT 191
                                                                                                                                                                                                GTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVH 251
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     71
                    12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KATO, NOBUO
APPLICANT: SAKAI, YOSHIKI
APPLICANT: TANI, YOSHIKI
APPLICANT: FUKUYA, HIROSHI
ITILE OF INVENTION: RECOMBINANT FRUCTOSYL AMINO ACID
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,059 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 0020-4253P
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
RICHARDA APPLICATION DATA:
APPLICATION NUMBER: 08/899,172
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
10S-09-031-059-3
'Sequence 3, Application US/09031059
'Patent No. 5948659
                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 FHDVKEWINVOYRDISKL 449
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APPLICANT: POLSYCH, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT PILING DATE: US 60/164415
PRIOR RILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 412
LENGTH: 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 EKTOIPKEAETRVRALLKETMPOLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 GASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMD
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                                                                                                                                                      12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
                                                               Gaps
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ilarity 23.0%; Pred. No. 3e-08;
Conservative 59; Mismatches 176; Indels 166;
                                                            1,
Length 437;
                                                            Indels
      DB 2;
                                                               33;
Query Match 78.4%; Score 1982.5; DB 2. Best Local Similarity 82.2%; Pred. No. 3.4e-194; Matches 360; Conservative 44; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 412, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
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US-09-711-164-412
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244 215 290 268	Qy 350 DTARREFLIRHPOYHSLVJGCGASGRCFKYLPSIGNLIVD-,	; Sequence 10219, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSON; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DISPITED OF THE REFERENCE: CLOODING AND MINDED. HEADOW, AND ICAMADON MINDED. HEADOW AND ICAMADON MINDED.	CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR PILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR PILING DATE: 2000-10-03 PRIOR PILING DATE: 2000-10-03 PRIOR PILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012	r Windows V	Ouery Match 5.9%; Score 150; DB 4; Len Best Local Similarity 20.8%; Pred. No. 6.4e-06; Matches 102; Conservative 77; Mismatches 187; II Qy 2 GGSGDDDIALAVTKSSSILIVGACTWGTSTALHIARRG' Db 31 GREGEEKPPLSAETQWKDRAETVIGGGCVGVSLAYHLAKRG	Qy 59 GNDVNKVISSGQYSNNKDEIEVNEILAL	Db 129 FHQPGSIRLATTPVRVDEFKYQMTRTGWHATEQYLIEPEKIQ) Qy 157 WKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRV Db 187NPGIGHIDPYSLTMALAAGARKCGALLKYPAF	217 238 273	Db 297 SYYLRQERDGLIFGPYESQERGKUQDSWVINGVPPGFGKELFP Qy 317 PKEABTRVRALLKETWPQLADRPFSFARICWCADTANREFLII Db 350 -KAAMEMVPVLKKADIINVVNGPITVSPDILPMV Qy 377 GFKYLPSIGNLIVD-AMEGKVPQKIHELIKWNPDIAANRNWRI
	118 -LVAEAEKEGVECIPGATVDALYEENGRVCGVICGD-DILRARYVVLAEGGA 234 QFLDPFKNQLRPTAWTLVHIALKPEERALYKNI PVIFNIERGFFPEPDEERGEI	OY 287 -KICDBIRGYINWQSAG	OY 374 SGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGG-PNR 428	RESULT 4 US-09-457-302-1 ; Sequence 1, Application US/09457302 ; Patent No. 6228626 ; GENERAL INFORMATION: ; APPLICANT: ICHIRAWA, Toshio	APPLICANT: KOYAMA, Yasuji TITLE OF INVENTION: SARCOSINE OXIDASE AND PROCESS FOR PRODUCING THE SAME FILE REPERENCE: 081356/0139 CURRENT APPLICATION NUMBER: US/09/457,302 CURRENT FILING DATE: 1999-12-09 EARLIER PILING DATE: 1998-12-14 MANDER OF COLD NOW.	ľΛ	US-09-457-302-1 Query Match Best Local Similarity 22.8*; Pred. No. 5.4e-07; Matches 94; Conservative 62; Mismatches 178; Indels 78; Gaps 22;	QY 20 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE 79 1 ::	Oy 134 ELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAAAREAQRM 185 Db

OCIATED
DETECTION AND USES THEREOF Indels 124; Gaps 23; STMPQLADRPFSFARICWCA 349 || |EEETGQVVG------ 128 VVTLIFENNDVKGAVTGDG 216 KPEERALYKNIPVIFNIE- 272 RDTLGRFGGPNRVMDFHDV 435 ERGFFFE-PDEERGEIKIC 289
| | :: | :| |
ENGIYYGFPSFGGSGLKI- 267 AEEAFN--GWKNDPLFKPY 101 --OSADGTWMSIPFEKTOI 316 PESDLDRIMEHI----- 349 IDRHPQYHSLVLGCGASGR 376 : | : | | IVGPHQGVRNYWVAIG-FGY 399 GYTNVTVLDPYPVPSAISA 58 -AMEGKVPOKI 400 ngth 866;

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APPLICANT: Cac, All Eliana
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VINULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT PILING DATE: 1998-11-25
PRIOR PILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VRVRPGEDPNLVELTRPEQFRKLAPEGVL------QGDFPGWK
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4%; Score 136.5; DB 4;
Best Local Similarity 22.9%; Pred. No. 4.2e-05;
Matches 96; Conservative 44; Mismatches 163;
              CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 5
LENGTH: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 367, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ausubel, Frederick APPLICANT: Goodman, Howard M. APPLICANT: Goodman, Howard M. APPLICANT: Rahme, Laurence G. APPLICANT: Mahajan-Miklos, Shalina
FILE REFERENCE: 020552-001410US
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tan, Man-Wah
Cao, Hui
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                              Sequence 21043, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 VESLGGRIYEQSPATRI-----ERGASPVVHTPQGKV---KAKFIVVAGNA--YLN---- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 GYTNMVQSADGTMMSI----PFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yu, Ming
APPLICANT: Sakowicz, Roman
APPLICANT: Batel, Umesh A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 146.5; DB 4; Length 448;
23.7%; Pred. No. 5.1e-06;
Live 59; Mismatches 164; Indels 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beraud, Christophe
APPLICANT: Craven, Andrew
APPLICANT: Yu, Ming
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-KWTTTQYTE 442
                      436 KEWTNVQYRD 445
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Best Local Similarity
Matches 98; Conserv
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US-09-252-991A-21043
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: | | : | | : | | : | | 175 IREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAIFQI-FVK 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 -----DFHDVKEWTNVQYRDISK---LKG--ELEGLPIPNPLL-----RTGHHHHHH 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 -----GYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 FVFDRVFGEAATOQDVFQHTTHSVLDSFLQGYNCSVFAYGATGAGKTHTMLGRE----- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 --GDPGIMYLTTVELYRRLEARQQEKHPEVLISYQEVYNE-----OIHDLLEPKGPLA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 TOIPKEAETRVRALLKETMPOLADRPFSFARICWCADTANREFLIDRHPOYHSLVLGCGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 QODRVPGLTQAVQVAKMSL-------1DLAGSERASSTHAKGERLREGANI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 VTGDGKIWRAERTFLCAGASAGO-----FLDFKNOLRPTAWTLVHIALKPEERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 12 VRVRPPTPRELDSQRRP--VVQVVDERVLVFNPEEPDGGFPGLKWGGTHDGPKKKGKDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 YKNIPVIFNIERGF-FFEPDEERGEIKIC-----DEHPGYTNMVQSADGTMMSIPFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 N-RSLLALINVLNALADAKGRKTHVPYR------DSKLTRLLKDSLG--GNCRTVMI
                                                                                                                                                                                                                                                                                                        Gaps
   OTHER INFORMATION: Description of Artificial Sequence: HsKip3a OTHER INFORMATION: fragment OTHER INFORMATION: OTHER INFORMATION: the ATPase assay (Figure 4).
                                                                                                                                                                                                                                                                                                    117;
Description of Artificial Sequence: HsKip3a
                                                                                                                                                                                                                              Length 383;
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19;

290

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 24053
LENGTH: 484
      ---TRPEQFRKLAPEGVLQGDFPGWKGYFARS--GAGWAHARNA 174
                                                                                                                  264 L-----LKPLGLELPVVPVK-GQMILYKCAADFLPRWV-LAKGRYAIPRRD-GHILIGS 314
                                                                                                                                                                                                                                                              291 --EHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLAD-----R 338
                                                                                                                                                                                                                                                                                                         -------FDKTPTDEALES-LRASAAELLPELADMQPVAHWAGLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAGEEQADVCVVGGGFSGVNTALELAQRGF-SVVLLEAHRIGWGASGRNGGQLIRGVGHD 135
                                             148 LYWLDLDDQTEALQWARKHTRP---LKEVPIEEAYAAVPGLGAGFQRAVYMSGVANVRNP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 RLGVRVRPG-----EDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGAGW 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LANKPGDYQGFREDMEELQALGYRHEMRLVPAAEMRSVVGSD--RYVGGLVDMGSGH 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 AHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 EERGEIKICDEHPGYTNMVQSADGTMM--SIPFEKTQIPKEAETRVRALLKETMPQLADR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 PFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEG---- 394
                                                                                                                                                                                                                                                                                                                                                 339 PFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVP 397
                                                                                                                                                                                                                                                                                                                                                                                 FLDFKNOLRPTAWTLVHIALKPEERALYK----NIPVIFNIERGFFFEPDEERGEIKICD
                                                                                       LVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAIS------AGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VNK---VISSGOYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSOEGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 GCNA----YMNDLNPLLGGKVLPAGSYV-IATEPLDEQLARQLLP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%; Score 134.5; DB 4; Best Local Similarity 22.4%; Pred. No. 9.7e-05; Matches 103; Conservative 70; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24053, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         315 TLEHSG-
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TITLE OF INVENTION: AUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                  77 EIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL--- 132
                                                                                                                                                                                                                                                                                                                                               -----AVTALAHWSQD--FYP-----ALGQRLLDBTGL-----DPEVHTVG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                107 LYWLDLDDQTEALQWARNHTRP---LKEVPIEBAYAAVPGLGAGFQRAVYMSGVANVRNP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 FLDFKNOLRPTAWTLVHIALKPEERALYK----NIPVIFNIERGFFFEPDEERGEIKICD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 L-----LKPLGLELPVVPVK-GQMILYKCAADFLPRWY-LAKGRYAIPRRD-GHILIGS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --EHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLAD-----R 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---VEL-------TRPEQFRKLAPEGVLQGDFPGWKGYFARS--GAGWAHARNA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 EIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNL--- 132
                                                                                                                                                                                                                                        -----AVTALAHWSQD--FYP-----ALGQRLLDETGL-----DPEVHTVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 PGSPEGIPY-----IGPVPGFDGLWLNTGHYRNGLVLAPASCRLLADLMSGREP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVP 397
                                                                                                                                                                                                               17 SSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 107;
                                                                                                                                                                    45; Mismatches 165; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 135.5; DB 4;
24.3%; Pred. No. 6.1e-05;
tive 45; Mismatches 165;
                                                                                                                           Score 135.5; DB 3
Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 21423, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
             LENGTH: 378
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                              5.4%;
                                                                                                                                                                    Matches 102; Conservative
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Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 TLEHSG-----
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-252-991A-21423
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                                                                              US-09-199-637A-367
SEQ ID NO 367
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                                                                                                                         Query Match
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321 -RGAFSDIRPVINYYRVTRE-----NRLLFGSATRF---VEYT--PNDFAAWNRTLLAEV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                     59 GNDVNKVISSGQYSNNKDEIE-----VNEILAEEAFNGWKNDPLFKPYYHDTGLLMSA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 CSQEGLDRLG-----VRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AGWAHARNALVAAAREAQRMGVKFVTGTP------QGRVVTLIFENNDVKGAVTGDGK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| : :| : | : | : | 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GHDIEAV----KKHVGKEGLETLFKIANLGAGIIRERIRKYNIDADFVPGY---GYL--A 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 IWRAERTFLCAGASAGQFLDFKNQLRPTAW--TLV----HIALKPEERALYKNIPVIFNI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 ERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKET 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 GGQIHSLAMALLGSAQAAHSLGVKIFESSPVVEVNYGKQVRVRTAM------GSVKAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 SSLLIVGAGTWGTSTALHL----ARRGYTNVTVLDPYPVPSAISAGNDVNKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 MPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNL 387
                                                                                                                                                                                                                                                                                                                                                         Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dennis J. Slamon
APPLICANT: Juliana J. Oh
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES
TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES
TITLE OF INVENTION: ASSOCIATED WITH HER-2/NEU OVEREXPRESSION
FILE REFERENCE: 30448.7905U1
CURRENT APPLICATION NUMBER: US/09/684,405
CURRENT ELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/157,923
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 486
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TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                          Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 486;
                                                                                                                                                                                                                                                                                                        4.9%; Score 124.5; DB 4;
22.6%; Pred. No. 0.001;
tive 48; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.9%; Score 123.5; DB 4;
Best Local Similarity 20.9%; Pred. No. 0.0013;
Matches 94; Conservative 53; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                     11 ALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPY
              FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000.01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09684405
Patent No. 6770477
                                                                                                                                                                                                             TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.6%
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                 US-09-489-039A-12890
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30872
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18-09-12890
18-09-489-039A-12890
2 Sequence 12890, Application US/09489039A
2 Patent No. 6610836
3 FARENT INFORMATION: A PAREON et. al
3 APPLICANT: Gary Breton et. al
4 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ACEMLDAARLRDLEP--VLR---PGLAGALKVPGDGILYAPN---AARWLLERA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 GYTNMVQSADGTMM------SIPFEKTQIPKEAETRVRALLK--ETMPQL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 GYVSSAHASSGTSVAFNAQPRPTGQVFLGSSRQFDTLDPQVEGPVLARMLRRALDYLPGL 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 DEIEVNEILAEEAFNGWKNDPLPKPYYHDTGLLMSAC-----SQEGLDRLGVRVR 125
  386 RIDYQWGGMIGIGANRLPQIGRLPGQPNVYFAQAYSGHGVNATHLAGQLLAEAIGGQQSD 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SSSLLIVGAGTWGTSTALHLARRGYTNVTVLDP-YPVPSAISAGNDVNKVISSGQYSNNK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 GVKFVTGTPQGRVVTLIFENNDVKGA--VTGDGKIWRAERTFLCAGASAGQFLDFKNQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 125; DB 4; Length 652; 21.8%; Pred. No. 0.0015;
                                                                           Sequence 30872, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 21.8 Matches 92; Conservative
                                                                                                                                                                 RESULT 11
US-09-252-991A-30872
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64 SDVVIVGGGVLGLSVAYWLKKGLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFSLPE 123
                                                                                                                    124 NIQLSLFSASFLRN----INEYLAV-----VDAPPLDLRFNPSGYLLLASEKDAAAME 172
                                                                                                                                                                              120 IGVRVRPGEDPNLVELTRPEOFRKLAP----EGVLQGDFPGWKGYFARSGAGWAHARNAL 175
                                                                                                                                                                                                                             173 SNVKVQRQEGAK-VSLMSPDQLRNKFPWINTEGVALAS-----YGMEDEGWFDPWCLL 224
                                                                                                                                                                                                                                                                                  176 VAAAREAQRMGVKFVTG------TPQGRVVTL------IFENNDVKG 210
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                                                                         ----ISSGOYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLD-R 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 VRALLK-----ETMPQLADRPFSFARI----CWCA----DTANREFLIDRHPQYHSL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |: : | | : : | 372 DPANLEVDHDFFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPHPLVVNM 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VWHCPQGPGLETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
PILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: V5HIS tagged
; OTHER INFORMATION: homo sapien
US-09-213-888-25
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US-09-328-877D-25
; Sequence 25, Application US/09328877D
; Patent No. 6730778
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APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FITLE OF INVENTION: Encode Them
FILE REPERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877D
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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ORGANISM: Artificial Sequence
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GenCore vereion 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	using sw model	May 27, 2005, 13:34:21 ; Search time 36.2303 Seconds (without alignments) 1253, 491 Million cell undates/sec
Copyright	OM protein - protein search, using sw model	Run on: May 27, 2005.
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Title: US-10-622-893A-5
Perfect score: 2530
Sequence: 1 MGGSGDDDDLALAVTKSSSL......LEGLPIPNPLLRTGHHHHHH 472

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Lipting first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

417 RDTLGRFGGPNR 428

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thiamin biosynthes	sarcosine oxidase	sarcosine oxidase	hypothetical prote	oxidoreductase ord	agaE protein (impo	probable oxidoredu	sarcosine oxidase	sarcosine oxidase	D-amino-acid dehyd	hypothetical prote	glucose inhibited	glucose-inhibited	glucose-inhibited	sarcosine oxidase	agaE protein (impo	
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652	417	417	442	442	437	452	396	413	420	703	629	629	629	405	441	
5.0	5.0	5.0	5.0	5.0	4.9	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	
126	125.5	125.5	125.5	125.5	123.5	116.5	114	114	113	113	112.5	112.5	112.5	112	111.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

57; SPDB:

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A;Gene: sox
C;Superfamily: sarcosine oxidase
C;Keywords: oxidoreductase
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Best Local Similarity
Matches 97; Conserv
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A; Residues: 1-389 <SUZ>
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A, Realdues: 1-433 <MCD>
A, Cross-references: UNIPROT: Q9UTM9; EMBL: AL132667; PIDN: CAB59618.1; GSPDB: GN00066; SPDB:
A, Experimental source: strain 972h-; cosmid c139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSOLUTED STATES OXIDASE (EC 1.5.3.1) - Bacillus sp.

Sarcosine oxidase (EC 1.5.3.1) - Bacillus sp.

Sispecies Bacillus sp.

C;Deccession: 139975

R;Suzuki, K.; Sagai, H.; Imamura, S.; Sugiyama, M.

J; Ferment. Biceng. 77, 231-234, 1994

A;Title: Cloning, sequencing, overexpression in Escherihia coil of a sarcosine oxidase-A;Reference number: 139975

A;Reference number: 139975

A;Reference number: 139975

A;Retatus: preliminary; translated from GB/EMBL/DDBJ
                                                                                              probable fructosyl amino acid oxidase - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T37605 R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Saunders, D.; Harris, D. submitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEYVCNVETDYDENSKVVSIPHSGPSKSSLPKYAIIQMRRFLDTFLPDLADRSLINTKMC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 GQFLDFKNOLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIKICDEH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 PGYTNMVQS---ADGTMMSIPF---EKTQIPKEAETRVRALLKETMPQLADRPFSFARIC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVPQKIHELIKW 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DPNLVELTRPEOFRKLAP----EGVLOGDFPGWKGYFARSGAGWAHARNALVAAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAQRMGVKFVTGTPQGR----VV----TLIFENNDVKGAVTGDGKIWRAERTFLCAGASA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 SSSLLIVGAGTWGTSTALHLAR-RGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
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                                                                                                                                                                                                                                                                                                                                                                                              18.4%; Score 465; DB 2; Length 433; 30.1%; Pred. No. 1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                80; Mismatches 174; Indels
                                                                                                                                                                                                    A;Reference number: 221729
A;Accession: T37605
A;Status: preliminary; translated from GB/EMBL/DDBJ
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| | | : |
R-----AGPSR 408
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A,Gene: SPDB:SPAC139.04c
A,Map position: 1
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Best Local S
Matches 130
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R;Suzuki, K.; Ogishima, M.; Sugiyama, M.; Inouye, Y.; Nakamura, S.; Imamura, S.
Biosci. Biotechnol. Biochem. 56, 432-436, 1992
A;Title: Molecular cloning and expression of a Streptomyces sarcosine oxidase gene in St.
A;Reference number: JS0671; MUID:92330009; PMID:1368326
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C,Comment: This enzyme catalyzes the oxidation of sarcosine to form formaldehyde, glycine
A;Residues: 1-390 <RES>
A;Cross-references: UNIPROT:P40859; GB:D16521; NID:g984787; PIDN:BAA03967.1; PID:g984788
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 ----LALRSQELWYE--LEKETHHKIFTKTGVLV------FGPK---GESAFVAET 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TRPEQFRKLAPEGVLOGD-----FPGW---KGYFA--RSGAGWAHARNALVAAAREAORM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 GVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPT 245
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C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
C.Accession: JS0671; PS0345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 VNEILAEEAFNGWKNDPLFKPYYH----DTGLLMSACSQEGLDRLGVRVRPGEDPNLVEL
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22.9%; Pred. No. 2e-06;
ative 59; Mismatches 150; Indels 128; Gaps
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A;Experimental source: strain KB210-8SX
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C;Keywords: oxidoreductase
F;2-389/Product: sarcosine oxidase #status experimental <SAR>
F;11-16/Region: nucleotide binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 192; DB 2; Lularity 23.2%; Pred. No. 2.7e-07; Conservative 68; Mismatches 162;
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A,Molecule type: protein
A,Residues: 2-31,122-143,230-259,268-283 <SUZ1>
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us-10-622-893a-5.rpr

	RESULT 6 144248 sarcosine oxidase (EC 1.5.3.1) [imported] - Arthrobacter sp. (strain TE1826) c;Species: Arthrobacter sp. A;Variety: strain TE1826 C;Date: 21-dan-2000 #sequence_revision 21-Jan-2000 #text_change 12-Jul-2004 C;Accession: T44448 R;Nishiya, Y.; Toda, A.; Imanaka, T. Mol. Gen. Genet. 257, 581-586, 1998 A;Title: Gene cluster for creatinine degradation in Arthrobacter sp. TE1826. A;Reference number: 222735; MulD:98223334; PMID:9563845 A;Reference number: 222735; MulD:98223334; PMID:9563845 A;Reference number: DNA A;Residues: 1-389 <nis> A;Residues: 1-389 <nis> A;Residues: 1-389 <nis> A;Residues: 1-389 <nis> A;Experimental source: strain TE1826 C;Keywords: oxidoreductase</nis></nis></nis></nis>	Query Match	RESULT 7 B65058 fixC protein homolog b2766 - Escherichia coli (strain K-12) N;Contains: probable quinone reductase (EC 1.6.5) C;Species: Escherichia coli C;Species: Escherichia coli C;Accession: B65058 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
Qy 80 UNBILABEAFNGWKNDPLFKPYYHDTGLLMSACS-QEGLDRLGVRVRPGE 128	172 RNALVAAAREAQRAGVKE 150 ENWVAAHLQLATRQGAE. 231 SAGQFLDFKNQLRPTAWT 193 TAGQLICPGAWP 289 CDEHPGYTNWVQSADGTW 287 PERHPVYIWEDADGVC 328 LKGTMPQLADRFSFP 328 LKGTMPQLADRFSFP 295 ADHMSALIPDLPGTFLKD 295 GNLIVD-AMEGKVPQKI	PESULT S JUNEAU STATISTICAL STATEMENT 371 RESULT S JUNEAU S JU	OY 189 FVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRABRTFLCAGASAGQFLDFKNQLRPTAWT 248

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RESULT
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kossidues: 1-387 <KCV's
A;Cross-references: UNIPROT:P23342; GB:D10553; GB:D01067; NID:g216326; PIDN:BAA01410.1;
A;Experimental source: strain NS-129
C;Comment: This enzyme catalyzes the oxidation of sarcosine to generate formaldehyde, g1
C;Superfamily: sarcosine oxidase
C;Keywords: oxidoreductase
       A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Recession: B65058
A;Status: prelimity; nucleic acid sequence not shown; translation not shown
A;Residues: 1-433 <BLAT>
A;Cross-references: GB:AE000360; GB:U00096; NID:92367157; PIDN:AAC75808.1; PID:91789125;
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: fixC procein
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 SGRGFKY----LPSIGNLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGG-PNR 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 ALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KICDEHPG----YTNMVQSADG-----TMMSIPFEKTQIPKEAETRVRALLKET-- 331
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C;Species: Bacillus sp.
C;Species: Bacillus sp.
C;Dacession: JU0461
R;Koyama, Y.; Yamamoto-Otake, H.; Suzuki, M.; Nakano, E.
Agric. Biol. Chem. 55, 1259-1263, 1991
A;Fitle: Cloning and expression of the sarcosine oxidase gene from Bacillus A;Reference number: JU0461; MUID:91291342; PMID:1368683
                                                                                                                                                                                                                                                                                                                                                                                                          --SKNLSGGRL-----YTHALAE-----YTHALAE-LSLL
                                                                                                                                                                                                                                                                                                    1 MGGSGDDDDLALAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGN
                                                                                                                                                                                                                                                                                                                             DVNKVISSGQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GVRVRPGEDPNLVELTRPEQFRKLAPEG----VLQGDFPGWKGYFARSGAGWAHARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TPDGVTT-------FSSLQPGGESWSVLRARFDPW-------
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                         6.6%; Score 168; DB 1; Length 433;
23.0%; Pred. No. 2.4e-05;
ive 59; Mismatches 176; Indels 166;
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278 LEYGAHLVÞEGGLHSMPVQYAGNGWLLVGDALRSCVNT-
                                                                                                                                                                                                                                             Best Local Similarity 23.09
Matches 120; Conservative
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                         LCHDMEDD
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DB 2; Length 387;

Score 155;

6.1%;

Query Match

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A;Molecule_type: DNA
A;Residues: 1-433 <HAY>
A;Cross-references: UNIPROT:Q8X7T8; GB:BA000007; PIDN:BAB37044.1; PID:g13363092; GSPDB:GP
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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H.
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91081
A;Status: preliminary
                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DVNKVISSGQYSNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRL 120
                                                                                                                                                                                                                                                                                                                134 ELTRPEQFRKLAPEGVLQGDFPGWKG-----YFA--RSGAGWAHARNALVAAAREAQRM 185
                                                                                                                                                                                                                                                                                                                                                      113 SLEH-ELF-----EGKQLTD--RWAGVEVPDNYBAIFEPNSGVLFSENCIQAYRELAEAH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 PTAWTLVHIALKPE-----ERALYKN---IPV-IFNIERGFFFE-PDEERGEIKIC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 DEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCA 349
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                                                                                                                                                                                               80 VNEILAEEAFNGWKNDPLFKPYYHDTGLLM-----SACSQEGLDRLGVRVRPGEDPNLV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Cispecies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                   165 GATVLTYTPVEDFEVTEDLVTIKTAKGSYT-----ANKLVVSMGAWNSKLLSKLD---
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                                                                                 20 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE
                                                                                                                                                                                                                                                         65 F-ALRAQELWYELEKETHHK-IFTQTGVLVYGPKGGSAFVSETM------EAANIH
                                                                                                                                                                                                                                                                                                                                                                                                                        186 GVKFVTGTP--QGRVVTLIPENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTANREFLIDRHPOYHSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVPQKI 400
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22.6%; Pred. No. 0.00048;
tive 51; Mismatches 153;
                          62; Mismatches 178;
     22.8%; Pred. No. 0.00022;
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                               94; Conservative
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Matches 107; Conserv
Best Local Similarity
Matches 94; Conserv
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Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (strain C58, Dupon C; Species: Agrobacterium tumefaciens (C; Species: Agrobacterium tumefaciens (C; Species: Agrobacterium tumefaciens (C; Species: Agrobacterium tumefaciens (C; Species: Agrobacterium tumefaciens (C; Species: Agrobacterium tumefaciens (C; Spacession: Agrato, D.) (C; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Zhang, S. (Genthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001

A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                               ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Sarcosine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 22.2% Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: AB3160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ygcN [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Becherichia coli (5, Species: Bespecies: Bespecies: Bespecies: Br.) (5, Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew illar, L.; Grotbeck, EJ.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A,Reference number: A85480; MUID:21074935; PMID:11206551
A,Reference: PRS926
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-433 <STO>
A,Cross-references: UNIPROT:Q8X7T8; GB:AEO05174; NID:g12517227; PIDN:AAG57874.1; GSPDB:G A,Experimental source: strain O157:H7, substrain EDL933
C,Genetics:
A,Gene: ygcN
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                             218 GGICDDLPGGAFLYTNQQTLSLGIVCPLSSLTQSRVPASELLARFKTHPAVRPLIKNTES 277
                                                                                                                                                                                          -- CADTANREFLIDRHPQYHSLVLGCGA 373
                                                                                                                                                                                                                                       LEYGAHLVPEGGLHSMPVQYAGNGWLLVGDALRSCVNT-------GI 317
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                                                                                         -KICDEHPG----YTNMVQSADG-----TMMSIPFEKTQIPKEAETRVRALLKET-- 331
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A;Residues: 1-380 «KUR»
A;Cross-references: UNIPROT:Q8UKUS; GB:AE008687; PIDN:AAL45696.1; PID:g17743424; GSPDB:G:
A;Experimental source: strain C58 (Dupont)
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Avature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoral A;Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 IRVILLEEFFALGGVLVTDQGAARV---MLEGGRAVGAETAEGYLHRADAVVLATGPAVPK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLG----VRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 RLSAGDVARVTPGIDAGAI-----TPQGAI-----FNPGEGWVDLPTL 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 MVGESGÓIIGDG---TPIALLVQTKPLAHPLRAVLNTPRVAVRPAPGGSFSLDADWA---
                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 148; DB 2; Length 380;
22.2%; Pred. No. 0.00076;
tive 51; Mismatches 151; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 -ADE-----GVTVRADGTY------EIDDTIVAELLVEAAK----
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OY 179 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRA 221	Qy 324 VRALLKETMPQLADRPFSPARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPS 383 Db 349 VPVLKKADIINIVNGPITYSPDILPMVGPHQGVRNYWVAIG-FGYGIIHAGG 399 Qy 384 IGMLIVD-AMEGKVPQKIHELIKMNPDIAANRNWRDTLGREGGPNRVMDFHDVKEWTNVQ 442 I	RESULT 14 B83078 probable D-amino acid oxidase PA4548 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004 C;Accession: B83078 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004 C;Accession: B83078 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Reference number: A82950; MUD:20437337; PMID:10984043 A;Accession: B83078 A;Status: preliminary A;Accession: B83078 A;Status: preliminary A;Accession: B1364 <sto> A;Cross-references: UNIPROT:P93642; GB:AE004868; GB:AE004091; NID:g9950785; PIDN:AAG07936' C;Genetics: A;Gene: PA4548 C;Superfamily: Sarcosine oxidase</sto>	Query Match 5.5%; Score 139.5; DB 2; Length 364; Best Local Similarity 24.6%; Pred. No. 0.0033; 103; Conservative 44; Mismatches 165; Indels. 107; Gaps 19; QY 17 SSLLIVGAGTWGTSTALHLARRGYTNVTUDDPYDPSAISAGNDVNKYISSGQYSNNKD 76 Db 2 SERVVVVGAGVIGLLTARELALAGLRVTLVERGESGREASWAGGGIVSPLYPWRYSP58 QY 77 BIEVNBILLAEBARNGWRNDPLFKPYYHDTGLLMSACSGGGIDRLGWRYPRGEDDNL132 Db 59AVTALAHWSQDFYPALGGRLDETGLDPEVHTVG 92 QY 133VELTRPEQFRKLAPEGVLQGDFFGWKGYFARSGAGWAHARNA 174 Db 93 LYWLDLDDGTEALQWARKHTRPLKEVPIEERAYAAVPGLGAGFQRAVYMSGVANVRNP 149 QY 175 LVAAAREAQRWGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKINRAERTFLCAGASAGQ 234 CY 15 LVAAAREAQRWGVKFVTGTPQGRVVTLIFENNDVKGAVTGSGCIARAERTFLCAGASAGQ 234 CY 15 LDFKNQLRFTAWTLVHIALKFEERALYKNIPVIENIERGFFFEPDEERGEKKCD 290 CY 235 FLDFKNQLRFTAWTLVHIALKFEERALYKNIPVIENIERGFFFEPDEERGEKKCD 290 CY 235 FLDFKNQLRFTAWTLVHIALKFEERALYKNIPVIENIERGFFFEPDEERGEKKCD 290 CY 235 FLDFKNQLRFTAWTLVHIALKFERALTYK
A;Status: preliminary A;Molecule type: DNA A;Rosidues: 1.427 <stod 0.0012;="" 164;="" 23.7%;="" 23;<="" 59;="" 93;="" 98;="" a;cross-references:="" a;experimental="" a;gene:="" best="" c;genetics:="" c;superfamily:="" conservative="" cuery="" gaps="" gb:ae004091;="" gb:ae004705;="" hi0499="" hypothetical="" indels="" local="" match="" matches="" mismatches="" nid:g9948851;="" no.="" pa01="" pa2776="" pidn:aag0616="" pred.="" protein="" similarity="" source:="" strain="" td="" uniprot:q91067;=""><td>Qy 18 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPPVBAISAGNDVNKVISSGQYSNNKDE 77 : :: </td><td>AKRIREVVATD VITLIFENNDVKGAV VITLIFENNDVKGAV IERGASPVVH II I</td><td>C; Accession: S1613; M; Brandsch, R. Eur. J. Biochem. 198, 793-799, 1991 A; Title: Rat liver dimethylglycine dehydrogenase. Flavinylation of the enzyme in hepatoc A; Title: Rat liver dimethylglycine dehydrogenase. Flavinylation of the enzyme in hepatoc A; Reference number: S1613; MulD: 91266966; PMID:1710985 A; Accession: S1613; MulD: 91266966; PMID:1710985 A; Accession: S1613; MulD: 91266966; PMID: 1710985 A; Accession: S1613; MulD: 91266966; PMID: 9126689; PIDN: CAA39468.1; PID: 91266896 C; Keywords: flavoprotein; oxidoreductase C; Keywords: flavoprotein; oxidoreductas</td></stod>	Qy 18 SSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPPVBAISAGNDVNKVISSGQYSNNKDE 77 : ::	AKRIREVVATD VITLIFENNDVKGAV VITLIFENNDVKGAV IERGASPVVH II I	C; Accession: S1613; M; Brandsch, R. Eur. J. Biochem. 198, 793-799, 1991 A; Title: Rat liver dimethylglycine dehydrogenase. Flavinylation of the enzyme in hepatoc A; Title: Rat liver dimethylglycine dehydrogenase. Flavinylation of the enzyme in hepatoc A; Reference number: S1613; MulD: 91266966; PMID:1710985 A; Accession: S1613; MulD: 91266966; PMID:1710985 A; Accession: S1613; MulD: 91266966; PMID: 1710985 A; Accession: S1613; MulD: 91266966; PMID: 9126689; PIDN: CAA39468.1; PID: 91266896 C; Keywords: flavoprotein; oxidoreductase C; Keywords: flavoprotein; oxidoreductas

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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-treferences: UNIPROT: Q9KB87; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB057
A;Experimental source: strain C-125
Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Sarcosine oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 VYPLKGQL--IVLKQGD----TDLNVMINTSKGYILSKPNGTVVLGATSEKEKFNKFI-T 279
|:|| |:|| |:|| |:|| |-----FDKTP-TDEAQESLRASAAELL.PELLADMQPVAHWAGLR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 EVNEILAEEAFN---GWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPG---EDPNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 ADGTMMSIP-FEKTQIPKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 VELTRPEQFRKLAP-----EGVLQGDFPGWKGYFARSGAGWAHARNALV--AAAREAQR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 MGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASA---GQFLDFKNQ 241
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                                                                                  339 PFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVDAMEGKVP 397
                                                                                                                          303 PGSPEGIPY------IGPVPGFDGLWLNTGHYRNGLVLAPASCRLLADLMSGREP 351
                                                                                                                                                                                                                                                                          hypothetical protein BH2041 (imported) - Bacillus halodurans (strain C-125)
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Sequence 13083, A
Sequence 6, Appli
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Sequence 13788, A
Sequence 13787, A
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9986, Ap
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Sequence 4818, Ap
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1. /cgn2 6/ptodata/2/paa/NCOE NEW COMB.pep:*
2. /cgn2 6/ptodata/2/paa/USOE NEW COMB.pep:*
3. /cgn2 6/ptodata/2/paa/USO7 NEW COMB.pep:*
4. /cgn2 6/ptodata/2/paa/USO7 NEW COMB.pep:*
5. /cgn2 6/ptodata/2/paa/USO9 NEW COMB.pep:*
6. /cgn2 6/ptodata/2/paa/USO9 NEW COMB.pep:*
7. /cgn2 6/ptodata/2/paa/USI0 NEW COMB.pep:*
8. /cgn2 6/ptodata/2/paa/USI1 NEW COMB.pep:*
GenCore version 5.1.6
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US-10-990-328A-13084

US-10-990-477-6

US-10-990-477-6

US-10-990-328A-13788

US-10-990-328A-13788

US-10-990-328A-13787

US-10-990-328A-13787

US-10-990-328A-13787

US-10-990-328A-13787

US-11-966-9120

US-11-0960-9120

US-11-096-086-33

US-11-040-686-34

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US-10-996-104A-22
US-11-031-175-9986
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Maximum Match 100%
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Sequence 20, App	Sequence 58, App	Sequence 15, App	Sequence 10, App	Sequence 10, App	Sequence 48529,	Sequence 36, App]	Sequence 42, Appl	Sequence 17883,	Sequence 18, Appl	Sequence 18, App.		Sequence 44587,	Sequence 44, Appl	Sequence 10, App]	Sequence 12, App	Sequence 40, App	Sequence 6, Appl	Sequence 6, Appl	Seguence 42765.
Sedn	Sedn	Sedn	Sedu	Sedu	Sedu	Sedu	Sedn	Sedu	Sedu	Sedn	Sedn	Sedu	Sedu	Sedu	Sedn	Sedu	Sedu	Sedu	Segn
US-10-996-104A-20	US-10-204-639-58	US-10-532-053-15	PCT-US05-04621-10	US-11-057-027-10	US-10-450-763-48529	US-60-645-354-36	US-11-040-686-42	US-60-643-717-17883	PCT-US05-10680-18	US-11-096-051-18	US-60-643-717-7212	US-10-450-763-44587	US-60-645-354-44	US-11-122-943-10	US-11-122-943-12	US-60-645-354-40	PCT-US05-02996-6	US-11-046-644-6	US-11-097-143-42765
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4.4	4.4	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1
112.5	111.5	109	108.5	108.5	108	107.5	107	106.5	105.5	105.5	105.5	105	104.5	104.5	104.5	104	104	104	104
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                     Length 459;
Sequence 13558, Application US/60643717
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REPERENCE: 38-21(53629)A
CURRENT APPLICATION NUMBER: US/60/643,717
CURRENT FILING DATE: 2005-01-12
NUMBER OF SEQ ID NOS: 19247
SEQ ID NO 13558
                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 226.5; DB 8;
19.8%; Pred. No. 1.2e-10;
tive 38; Mismatches 101;
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; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-60-643-717-13558
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Matches 90; Conserv
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; ORGANISM: Homo sapiens
US-10-990-328A-13084
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DREADS.
TITLE OF INVENTION: DREADS.
TITLE OF INVENTION OF 10,000 OR MORE
TITLE OF INVENTION NUMBER: 06/11/097,143
CURRENT APPLICATION NUMBER: 06/157,832
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 66/161,932
PRIOR APPLICATION NUMBER: 66/161,932
PRIOR PLILING DATE: 1999-10-28
PRIOR PLILING DATE: 1999-11-12
PRIOR PLILING DATE: 1999-12-28
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PRIOR PLILING DATE: 1999-12-28
PRIOR PLILING DATE: 1999-12-28
PRIOR PLILING DATE: 1999-12-28
PRIOR PLILING DATE: 1999-12-38
PRIOR PLILING DATE: 2000-02-24
PRIOR PLILING DATE: 2000-03-23
PRIOR PLILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRACKED FOR WINDOWS VETSION 1-10
PRIOR PLILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRACKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 NELGAR-----NELLGPEALRORFPWLSTEGVELGCHGIDKEGWFD------PWA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 HARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENND---VKGAVTGDGKIWRAERTF- 225
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24.1%; Pred. No. 6.7e-07;
Live 57; Mismatches 149; Indels 135;
                                              427 NRVMDFHDVKEWTNV-----QYRDISKLKGELEG 455
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Best Local Similarity 24.1*
Matches 108; Conservative
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ORGANISM: DROSOPHILA
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US-10-990-328A-13083
US-10-990-328A-13083
Sequence 13083, Application US/10990328A
SEQUENCE HORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
STILE REPRENCE: 2004-11-17
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT APPLICATION NUMBER: US/10/990,328A
SOFTWARE: FOSESO FOR WINDOWS VERSION 4.0
SEQ ID NO 13083
LENGTH. 445
                                                                                                                                                                                                                                                                                                                                                                      Sequence 13084, Application US/10990328A
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DOLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
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368 VLGCGASGRGFKYLPSIGNLIVD-AMEGK 395
                                                                  386 FIAAGFSGHGIQQTPAVGRAISELILDGK 414
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Sequence 1, Application US/10534583
GENERAL INFORMATION:
APPLICANT: KISHIMOTO, Takahide
APPLICANT: SOGABE, Ateushi
TILLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS
TILLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS
TILLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS
TILLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS
TILLE OF INVENTION: MODIFIED SARCOSINE OXIDASE, PROCESS
TILLE OF INVENTION: MUMBER: 2005-05-11
PRIOR APPLICATION NUMBER: DCT/JP2003/014423
PRIOR PILING DATE: 2005-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR PILING DATE: 2002-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR PILING DATE: 2003-11-13
PRIOR PILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-0-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTLY VERBION 3.1
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                                                                                                               RELAVAKGAKILIYT---RVEDFEVSQDQVK-IQTANGS-YTADKLIVSMGAMNSKLLSK 212
                                                                                                                                                                                                          213 IN-----LDIPLQPYRQVVGFFDSNEAKYSNDVDYPAFMVEVPKGIYYGFPSFGG- 262
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     : : : : : : - FEPNSGVLFSENCIRSY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                             179 AREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDF
                                                                                                                                                                             KNOLRPTAWTLVHIALKP-----BERALYKN---IPV-IFNIERGFFFEPDEERGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 SNNKDEIEVNEILAEEAFNGWKNDPLFKPYYHDTGLL-------MSACSOEGL
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                                                                                                                                                                                                                                                                                                                                                                             346 CWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVD-AMEGKVPQKI 400
                                                                                                                                                                                                                                                                                                                                                                                                       CMYTKTPDEHFVIDTHPEHSNVFVAAGFSGHGFKFSSVVGEVLSQLATTGKTEHDI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LAVTKSSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 169; DB 6; Length 389;
21.1%; Pred. No. 6.4e-06;
tive 69; Mismatches 171; Indels 100;
, ORGANISM: Arthrobacter SP. TE1826
US-10-534-583-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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hes 91; Conserva
                                                                                                                              158
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APPLICANT: KAJIYAWA, Naoki
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES, MODIFIED SARCOSINE OXIDASES
TITLE OF INVENTION: AND METHODS FOR PREPARING THE MODIFIED SCARCOSINE OXIDASES
FILE REFERENCE: 261714050
CURRENT APPLICATION NUMBER: US/10/990,477
CURRENT FILING DATE: 2004-11-18
PRIOR APPLICATION NUMBER: JP 2004-184960
PRIOR PAPLICATION NUMBER: JP 2004-184960
PRIOR PILING DATE: 2004-06-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 6
                                                                                                                              16;
                                                                                                                                                                                                       66 IVIGAGIQGCPTAYHLAKH-RKRILLLEQPFLPHSRGSSHGQSRIIRKAYLE----DF 118
                                                                                                                                                                                                                                                                          81 NEILAEBAFNGWKNDPLFKPYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLVELTRPEQ 140
                                                                                                                                                                                                                                                                                                                           119 YTRMMHECYQIWAQ-----LEHEAGTQLH--RQTGLLLLGMKENQELKTIQANLSRQRV 170
                                                                                                                                                                                                                                                                                                                                                                             141 FRKLAPEGVLQGDFP-----GWKGYFARSGAGWAHARNALVA---AARE---AQRMGVK 188
                                                                                                                                                                                                                                                                                                                                                                                                                 HOLLSSEELKQRFPNIRLPRGEVGLLDNSG-GVIYAYKALRALQDAIRQLGGIVRDGEK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 FVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 VVBINP-GLLVT-----VKTTSRSYQAKSLVITAGPWTNQL-----LRPLGIE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLGVRVR PGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 LVHIALKPEERALYKNIPVIPNIERGF------FFEPDEERGEIKICDEHPG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 YTNMVQSADGTMMSIPFEKTQIPKEAETRV-RALLKETMPQLADRPFSFARICWCADTAN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 F-ALRAQELWYELENETHNK-IFTKTGVLVFGPKGESDFVAETWEAAAEHSLTVDLLEGD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE 79
                                                                                                                              Gaps
                                                                                                                                                                          21 LIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIEV
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                                                                             Length 445;
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                                                                           ; Score 177.5; DB 6; Length 4; Pred. No. 1.5e-06; 66; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 REFLIDRHPOYHSLVLGCGASGRGFKYLPSIGNLIVD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 VNEILAEEAFNGWKNDPLFKPYYHDTGLL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/10990477; GENERAL INFORMATION:
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                                                                           7.0%;
                                                                                                  1 Similarity 21.7986; Conservative
  ; ORGANISM: Homo sapiens
US-10-990-328A-13083
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                                                                           Query Match
Best Local S
Matches: 86
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Best Local 9
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23;

Gaps

58

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Sequence 13787, Application US/10990328A
GENERAL INFORMATION:
SEQUENCE 13787, Application US/10990328A
GENERAL INFORMATION:
SEQUENCE INFORMATION:
Michele
TITLE OF INVENTION:
USES THEREOF
FILLE REFERENCE:
CLOO1495
CURRENT APPLICATION NUMBER: US/10/990,328A
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13787
                             JENERAL INTOLUCIA:
JENERAL INTOLUCIA:
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JENERAL INTOLUCIA:
JENERAL INTERPLEMENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: BROODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL001495
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 13788
LENGTH: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 GFKYLPSIGNLIVD-AMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GN-------DVNKVISSGQYSNNKDBIEVNEILAEEAFN--GWKNDPLFKPY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 YHDTGLIMSACSQEGLDRLGVRV-RPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 KIWRAERTFLCAG---ASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIE- 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 -----RGFFFEPDEERGEIKICDE-----HPGYTNWV--QSADGTMMSIPFEKTQI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 PKEAETRVRALLKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 -----npgdghidpysltmalaagarkcgallkypap---vtslkarsdgtwdvetpog
                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 WKGYFARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 SYYLRQERDGLLFGPYESQEKMKVQDSWVTNGVPPGFGKELFESDLDRIMEHI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 -KAAMEMVPVLKKADIINVVNGPITYS-----PDILP---MVGPHQGVRNYWVAIG-FGY
                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGSGDDDLALAVTK---SSSLLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISA
                                                                                                                                                                                                                                                                                                                                            5.9%; Score 150; DB 6; Length 774;
20.8%; Pred. No. 0.00066;
trive 77; Mismatches 187; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10990328A
                                                                                                                                                                                                                                                                                                                                                                                        Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 KEWTNVQYRD 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| || :
-KWTTTQYTE 442
                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-990-328A-13788
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT: FURUKAWA, Naoki
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES,
TITLE OF INVENTION: MODIFIED SARCOSINE OXIDASES
FILE REFERENCE: 261714US0
CURRENT APPLICATION NUMBER: US/10/990,477
CURRENT APPLICATION NUMBER: US/2003-387975
PRIOR FILING DATE: 2004-11-18
PRIOR FILING DATE: 2004-11-18
PRIOR FILING DATE: 2004-06-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.2
SEOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLGVRVRPGEDPNLVELTRPEQFRKLAPEGVLQGDFPGWKGYFARSGAGWAHARNALVAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 KNOLRPTAWTLVHIALKP------EERALYKN---IPV-IFNIERGFFFEPDEERGE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 IKICDEHPGYTNMVQSADGTMMSIPFEKTQIPKEAETRVRALLKETMPQLADRPFSFARI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 EINTR-WPG-----ITVPENYNAI--------FEPNSGVLFSENCIRSY 157
    247 FWVEVPTGIYYGFPSFGGCGLKIGYHTYGQKIDPDTINREF---GIYPEDEGNIRKFLET 303
                                                              TMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSIGNLIVD 390
                                                                                     304 YMPG-ATGELKSGAVCMYTKTPDEHFVIDLHPQFSNVAIAAGFSGHGFKFSSVVGETLSQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LLIVGAGTWGTSTALHLARRGYTNVTVLDPYPVPSAISAGNDVNKVISSGQYSNNKDEIE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 165; DB 6; Length 387; Pred. No. 1.4e-05; 68; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-990-477-2
                                                                                                                                                                                                                                                RESULT 7
US-10-990-477-2
; Sequence 2, Application US/10990477
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICANT: KIKKOMAN CORPORATION APPLICANT: FURUKAWA, Keisuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          match 6.5%;
Local Similarity 21.4%;
les 89; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                              391 -AMEGKVPOKI 400
                                                                                                                                                                                     з6з гАУТСКТЕНDі 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 WKGYPARSGAGWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDG 216
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### TITLE OF INVENTION: MFTHOD OF TARGETED GENE DISRUPTION, GENOME OF
### TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
### TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
### TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
### TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
### CURRENT FILING DATE: 2005-02-39
### PRIOR FILING DATE: 2003-08-30
### PRIOR PLIING DATE: 2003-08-30
### PRIOR PLIING DATE: 2003-08-30
### PRIOR PLIING DATE: 2002-08-30
### PRIOR PLIING DATE: 2003-08-30
### SEQ ID NO 372
### LENGTH: 388
### LENGTH: 388
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                                                                                                                                                                                                                 5.9%; Score 150; DB 6; Length 866;
20.8%; Pred. No. 0.00077;
tive 77; Mismatches 187; Indels 124;
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ORGANISM: Thermococcus kodakaraensis KOD1
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LOCATION: (414542)..(414542)
OTHER INFORMATION: n is a or c or
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                                                                                                                                                                                                                                                                      Best Local Similarity 20.8
Matches 102; Conservative
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-KWTTTQYTE 442
                                              ; ORGANISM: Homo sapiens
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US-10-526-324-372
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71 YSNNKDEIEVNEI-LAEEAFNGWKNDPLFKPYYHDTGLLMSACSQEGLD------R 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 ASAGQFLDFKNQLRPTAWTLVHIALKPEERALYKNIPVIFNIERGFFFEPDEERGEIK-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NALVAAAREAQRMGVKFVTGTPQGRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAG 229
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; OTHER INFORMATION: n is a or c or g or t.
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LOCATION: (839139)..(839139)
OTHER INFORMATION: n is a or c or
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LOCATION: (1128488)..(1128488)
OTHER INFORMATION: n is a or c or
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LOCATION: (1128499). (1128499)
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LOCATION: (1128505)..(1128506)
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LOCATION: (1561477)..(1561477)
OTHER INFORMATION: n is a or c
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OTHER INFORMATION: n is a or c
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LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a or c
NAME/KEY: misc_feature
LOCATION: (786907)...(786907)
OTHER INFORMATION: n is a or
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LOCATION: (786944)..(786946)
OTHER INFORMATION: n is a or
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                                                                                                                                                                                                 G----NLIVDAMEGKVPQKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDVKEWTN 440
                                                     288 -ICDEHPGYTNMVQSAD-----GTMMSIPFEKTQIPKEAETRVRALLKETMPQLADR 338
                                                                                         ------PTYDFLRGV 290
                                                                                                                        339 PFSFARIC-------WCADTANREFLIDRHPQYHSLVLGCGASGRGFKYLPSI 384
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                                                                                     247 VISFKHGG-VYMTQEANQGGVIGGYGLKYGPTYDIT----
AWA-----PLINKWAGVPIKIPIEPYKHQSVKTEPI-
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; APPLICANT: Imanaka, Takayuki
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LOCATION: (839139)..(839139)
OTHER INFORMATION: n is a or c or
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LOCATION: (1128505)..(1128506)
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LOCATION: (414542)..(414542)
OTHER INFORMATION: n is a or
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LOCATION: (786944)..(786946)
OTHER INFORMATION: n is a or
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LOCATION: (786907)
OTHER INFORMATION: n is a or
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SEQ ID NO 29
LENGTH: 386
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US-10-526-324-29
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Sequence 20, Application PC/TUSO510680
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
FILE REFERENCE: Attorney Docket No. Cura 967
CURRENT APPLICATION TUMBER: PCT/USO5/10680
CURRENT FILING DATE: 2005-04-07
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208 WAKLINAMAGIRTKIPIEP----YKHQAVI------TQPIKKGSVKPMVISFRYGH 253
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LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a or c or g
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-----YVMDTLVMK 634
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                                                              256 PEER-----ALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMM 307
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                                                                                                                                           308 SIP----FEKTQIP-----KEAETRVRALLKETMPQLADRPFSFARI----
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TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
CURRENT APPLICATION NUMBER: US/10/800,077
CURRENT FILING DATE: 2004-03-12
PRIOR PELLING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
PRIOR FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 396
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 386
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                                                                                                   635 KEENDIPSCDLSGFVRPNPIIVSSPLSTFFRSSPEDSPI-
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                                                                                                                                                                                                                                                                                                                                                                                                        930 QOPPVVSSLEGKPIPNPLLGLDSTRTGHHHHH 862
                                                                                                                                                                                                                                                                                                                                                                             453 -----LEGLPIPNPLL----RTGHHHHHH 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 DISKLKGELEGLPIPNPLL----RTGHHHHHH 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 125.5; DE ilarity 23.0%; Pred. No. 0.05; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Recombinant B4ECv3 protein US-10-800-077-386
    | :||:|| : | :|
599 GASLTLVFERSPF---LTQYHTVWI PWNVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-60-669-241-28797
; Sequence 28797, Application US/60669241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 386, Application US/10800077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reddy, Ramachandra APPLICANT: Gill, Parkash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-800-077-386
                                                                                                                                                                                                                                                                                                   398
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                                                                                                                                                                                                                                                                                                                                           | :||:|| : :| : :| : | GASLTLVFERSPF----TLYYMIDWINVF---------YVMDTLVMK 634
                                                                                                                                                                                                                                                                                                                   196 GRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIALK 255
                                                                                                                                                                                                                                                                                                                                                                                               256 PEER-----ALYKNIPVIFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMM 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 SIP----FEKTQIP-----KEAETRVRALLKETMPQLADRPFSFARI----- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 ----CWCADTAN--REFLIDRHPQYHSLVLGCGAS--GRGFKYLPSIGNLIVDAMEGKVP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKIHELIKWNPDIAANRNWRDTLGRFGGPNRVMDFHDVKEWTNVQYRDISKLKGE---- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 ESCLDLTLWEKRTAILQGYELDASNMGG--WTLDKHHV---LDVQNGILYKGNGENQFIS 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 GRVVTLIFENNDVKGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIALK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 5.0%; Score 126.5; DB 7; Length 862; 1 Similarity 21.3%; Pred. No. 0.073; 71; Conservative 34; Mismatches 103; Indels 125;
                                                                                                                                                                                                                                                                                Indels 125;
                                                                                                                                                                                                                                        5.0%; Score 126.5; DB 1; Length 862; 21.3%; Pred. No. 0.073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 RLFQKWFPASPNLAYTFIWDKTDAYNQKVYGLSEAVVSVGYEY---
                                                                                                                                                                                                                                                                                                                                                                                                                          34; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 QOPPUVSSLEGKPIPNPLLGLDSTRTGHHHHHH 862
PRIOR APPLICATION NUMBER: US TO be assigned PRIOR FILING DATE: 2005-03-30 PRIOR FILING DATE: 2005-03-30 PRIOR PILING DATE: 2004-03-30 NUMBER OF SEQ ID NOS: 38 SOFTWARE: CLIRASeqList Version 0.1 SEQ ID NO 20 LENGTH: 86.2
                                                                                                                                                                                                                                                        Local Similarity 21.3
                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                  PCT-US05-10680-20
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                                                                                                                                                                                                                                          Query Match
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Best Local (
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318 KEAETRVRALLKETMPQLADR--PFSFARI--CWCA----DTANREFLIDRHPQYHSLVL 369
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
FILE REPERENCE: 38-21 (53596)
CURRENT APPLICATION NUMBER: US/60/669,241
CURRENT PILING DATE: 2005-04-07
PRIOR FILING DATE: 2004-04-09
PRIOR FILING DATE: 2004-04-09
PRIOR FILING DATE: 2004-04-27
PRIOR FILING DATE: 2004-04-27
PRIOR PILING DATE: 2004-06-11
PRIOR FILING DATE: 2004-06-10
PRIOR FILING DATE: 2004-06-10
PRIOR FILING DATE: 2004-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Homolog annotation: Hit ID=XP 319829.1; Match level="QueryCoverage OTHER INFORMATION: =97%, HitCoverage=96%, E-value=1e-136, Identity=45%"; Hit descrip; OTHER INFORMATION: ENSANGP0000015949 [Anopheles gambiae] PEATURE: CHER INFORMATION: Pfam annotation: Pfam ID=DAO; Match level="Score=211.2, B-value=2 OTHER INFORMATION: -60, Copies=1"; Pfam description=FAD dependent oxidoreductase US-60-69-241-28797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_3881; Strand=+; Position=84-
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 RGTHILQDNYNLQTSLGAK---VELLSPEKLKEKFPFMNTDGVA------LGCHGLENE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWFDPWSLLSAFKRKAVALGTEVV----NGKVTSFDFMNKSPIYNQYFAPGEYSHVEKAN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 HCPDAPGLAMPFIIDPTGAXVRREGVGGQYLCGISPGDEEQEPCCDN--MDVDXEFFE-- 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 ILIIGGGVMGFSIAYWLQQRALDHLRIVVVEQDPTVNP-----DKSKWLEYQKSTSVL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 SSG---QYSNNKDEIEVNEILAEEAFN----GWKN----DPLFKPYYHDTGLLMSACSQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 EGL----DRLGVRVRPGEDPNLVELTRPEQFRKLAP----EGVLQGDFPGWKGYFARSGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 GWAHARNALVAAAREAQRMGVKFVTGTPQGRVVTLIFENN-------D 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 VKGAVTGDGKIWRAERTFLCAGASAGQ---FLDFKNQLRPTAWTLVHIALKPEERALY-K 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 NIPVIFNIERGFFFEPD-----EERGEIKICDEHPGYTNMVQSADGTMMSIPFEKTQIP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 LLIVGAGTWGTSTALHLARRGYTNVTVL----DPYPVPSAISAGNDVNK------VI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.9%; Score 124.5; DB 8; Length 530; Best Local Similarity 21.4%; Pred. No. 0.055; Matches 94; Conservative 64; Mismatches 167; Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (519)..(519)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                      Baum, James A
Gilbertson, Larry A
Kovalic, David K
LaRosa, Thomas J
Lu, Maolong
Munyikwa, Tichifa R. I.
Roberts, James K
Wu, Wei
                                 Monsanto Technology LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Conservative
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SEQ ID NO 28797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Lygus hesperus
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434 ------NKLWPITANRVPAFECAKVKNAWSGFYDFNSFDENAFIGPHPAFHNVHV 482
                                                                        370 GCGASGRGFKYLPSIGNLIV 389
                                                                                                         483 VAGFSGHGIQQSPAVGRAMM 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: nucleotide sequence encoding a chimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yuan, Chong-Sheng
APPLICANT: Datta, Abhijit
APPLICANT: Datta, Abhijit
APPLICANT: Wang, Yuping
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
TITLE OF INVENTION: DETERMINATION OF GLYCATED PROTEINS
CURRENT APPLICATION NUMBER: 2003-07-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FESTESQ for Windows Version 4.0
SEQ ID NO 6
US-10-123-155-480
US-10-146-731-480
US-10-140-472-480
US-10-140-480-480
US-10-142-880-480
US-10-138-790-480
US-10-138-790-480
US-10-138-790-480
US-10-140-923-480
US-10-141-755-480
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US-10-140-805-480
US-10-140-805-480
US-10-140-805-480
US-10-140-805-480
US-10-140-805-180
US-10-140-805-180
US-10-140-805-180
US-10-140-478
US-10-140-478
US-10-140-478
US-10-141-761-478
US-10-141-759-478
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10622893A; Publication No. US20050014935A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 1419; Conserv
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Sequence 3, Appli
Sequence 4, Appli
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 9647, Ap
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                                                                                                                                        May 29, 2005, 21:41:14 ; Search time 921 Seconds (without alignments) 9459.321 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBZOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBZOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBZOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_PUBZOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10B_PUBZOMB.seq:*
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                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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9 US-10-470-678-1 ...
9 US-10-470-678-3 ...
9 US-10-470-678-4 ...
6 US-10-470-678-4 ...
6 US-10-232-655-4 ...
6 US-10-232-655-2 ...
10-232-655-2 ...
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Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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                          1201 CACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACCGTAACTGGGGTGATACTCTG
                                                                                       GGGCGTTTTTGGCGGTCCAAATCGTGTGATGGATTTTCATGATGTGAAGGAATGGACCAAT
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TITLE OF INVENTION: COMPOSITION FOR ASSAVING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P
CURRENT APPLICATION NUMBER: US/10/470,678
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: JP 2001/ 22953
PRIOR APPLICATION NUMBER: JP 2001/ 39796
PRIOR APPLICATION NUMBER: JP 2001/ 39796
PRIOR APPLICATION NUMBER: JP 2001/ 39796
PRIOR APPLICATION NUMBER: JP 2001/ 24002
PRIOR APPLICATION NUMBER: JP 2001/ 24002
PRIOR PRIOR DATE: 2001-02-16
PRIOR APPLICATION NUMBER: JP 2001/ 24002
PRIOR APPLICATION NUMBER: JP 2001/ 24002
PRIOR APPLICATION NUMBER: JP 2001/ 24002
PRIOR APPLICATION NUMBER: JP 2001/ 24002
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Best Local Similarity 55.3%; Pred. No. 3.4e-99;
Matches 721; Conservative 0; Mismatches 568;
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LOCATION: (1)..(1320)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: DDBJ E16562
DATABASE ENTRY DATE: 1999-07-28
PATENT DOCUMENT NUMBER: 1999-01-20
PATENT FILING DATE: 1997-01-20
PUBLICATION DATE: 1998-08-04
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ORGANISM: Fusarium oxysporum IFO-9722
FEATURE:
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US-10-470-678-1
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                                                 TATACCAACGTTACCGTGCTGGACCCCTATCCTGTCCTTAGCGCCCATCTCCGGCGGAAAC
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NAME/KEY: CD3
FEATURE:
NAME/KEY: mutation
NAME/KEY: mutation
LOCATION: (1115) .. (1115)
US-10-470-678-3
            APPLICANT: KOUZUMA, Takuji et al.
TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P
CURRENT APPLICATION NUMBER: US/10/470,678
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: UP 2001/22953
PRIOR APPLICATION NUMBER: UP 2001/39796
PRIOR PILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.2
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Pred. No. 1.1e-98;
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Matches 719; Conservative
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OTHER INFORMATION: sequence derived from Fusarium oxysporum IFO-9722
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TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
FILE REFERENCE: 1516-0121P
CURRENT APPLICATION NUMBER: US/10/470,678
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: UP 2001/ 22953
PRIOR PELING DATE: 2001-01-13
PRIOR PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: UP 2001/ 39796
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: UP 2001/ 24002
PRIOR PELING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 200
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| Sequence 4, Application US/10470678
| Publication No. US20050101771A1
| GENERAL INFORMATION:
| APPLICANT: KOUZUMA, Takuji et al.
| TITLE OF INVENTION: COMPOSITION FOR ASSAYING GLYCATED PROTEINS
| TILE REPERENCE: 1516-0121P
| CURRENT APPLICATION NUMBER: US/10/470,678
| CURRENT APPLICATION NUMBER: US/10/470,678
| CURRENT PILING DATE: 2001-01-13
| PRIOR PILING DATE: 2001-01-13
| PRIOR PILING DATE: 2001-02-16
| PRIOR PILING DATE: 2001-02-16
| PRIOR PILING DATE: 2001-02-16
| RIOR PILING DATE: 2001-03-08
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 4
| LENGTH: 1320
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Pred. No. 3.9e-98;
0; Mismatches 570; Indels
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Best Local Similarity 55.1%;
Matches 719; Conservative
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US-10-470-678-4
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US-10-470-678-4
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1184 AAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACCGTA 1243
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US-10-767-701-22052
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                                                                                                         1244 ACTGGCGTGATACTCTGG 1261
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Best Local Similarity 46.8%;
Matches 180; Conservative
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LENGTH: 422
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1211 TTACCGAGTTCTGGGGTAAAGATCCTCTGGATCGGTTTGGAGCTGACGATAAGATCATGG 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------CCGAAACGCGCGTTCGGGCCCTGCTGAAAGAGACAATGCCCCAGC 1003
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APPLICANT: HIROKAWA, KOZO
APPLICANT: HIROKAWA, KOZO
APPLICANT: HIROKAWA, NAOKI
TITLE GWINYENTION: NO. US200310157593Alel fructosyl peptide oxidase
FILE REFERENCE: 227590US0
CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR PILING DATE: 2001-09-04
PRIOR PELICATION NUMBER: JP 2001-378151
PRIOR FILING DATE: 2001-12-12
PRIOR PELICATION NUMBER: JP 2001-378151
PRIOR PELICATION NUMBER: JP 2002-228727
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-08-06
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                                                                            1271 ATTTGCCCAAGAGTGATGTAGAGGGATGGACAAATATCAAGAAT 1314
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Pred. No. 3.2e-09;
0; Mismatches 287; Indels
                                                                                                                                                                               ; Sequence 4, Application US/10232655; Publication No. US20030157593A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Eupenicillium terrenum US-10-232-655-4
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1314
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Matches 298; Conservative
                                                                                                                                                                                                         GENERAL INFORMATION
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RESULT 7
US-10-767-701-22052
Sequence 22052, Application US/10767701
Sequence 22052, Application US/10767701
Sequence 22052, Application US/10767701
Sequence 22052, Application US/10767701
Sequence 22052, Application No. US20040172684A1
Septicant: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
STILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
SUBRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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; Publication Wo. US20030157593A1
; Publication Wo. US20030157593A1
; Pablicanr. KUROSAWA, KEIKO
; APPLICANT: HIROKAWA, KOZO
; APPLICANT: KAJIYAWA, MOZO;
; TITLE OF INVENTION: No. US20030157593A1e1 fructosyl peptide oxidase
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Pred. No. 1.4e-07;
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GCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGACGCGATGGAAG 1180
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                                                                                                                                                                                                                         1181 GTAAAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACC 1240
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                                                                                                                                                                                                                                                                                                      31 GCTCTCGCCGTCACTAAGTCATCATCTCTCCTGATCGTTGGTGCCGGGACTTGGGGCCACC
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Pred. No. 0.92;
0; Mismatches 73; Indels 0
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APPLICANT: Oblien, Kari L.
APPLICANT: Oblien, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramanco, Robert T.
APPLICANT: Xu, H. Howard J.
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE REFERENT SLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR STILING DATE: 2000-05-23
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-01-23
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
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PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Best Local Similarity 52.6%;
Matches 81; Conservative
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ORGANISM: Salmonella typhi
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US-09-815-242-9647
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i Sequence 78, Application US/10600230

i Fublication No. US2040092020A1

i GENERAL INFORMATION:

APPLICANT: Wilkinson, Jack

APPLICANT: Wilkinson, Jack

APPLICANT: Westide, Kevin

TITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN

TITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN

TITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN

TITLE OF INVENTION: 3' POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN

FILE REFERENCE: 0325.210

CURRENT APPLICATION NUMBER: US/10/600,230

CURRENT PILING DATE: 2003-06-20

PRIOR PRIOR PILICATION NUMBER: 60/390,529

PRIOR PILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 78

LENGTH: 3731
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3.6%; Score 50.4; DB 16; Length 1314;
Best Local Similarity 52.3%; Pred. No. 4e-05;
Matches 136; Conservative 0; Mismatches 121; Indels 3;
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Pred. No. 0.48; ·
0; Mismatches 142; Indels 0;
                      CURRENT APPLICATION NUMBER: US/10/232,655
CURRENT FILING DATE: 2003-01-10
PRIOR PILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: JP 2001-378151
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-08-06
NUMBER: OF SEQ ID NOS: 24
SEQ ID NO 2
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; ORGANISM: Aspergillus nidulans
US-10-600-230-78
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Matches 124; Conservative
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FILE REFERENCE: 227590US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1314
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151 CCTGTCCCTAGCGCCATCTCCGCCGGAAACGACG 184
                                 187 carciregerarégegedecégecéaaacégee
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-112-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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Pred. No. 0.9;
0; Mismatches
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25526
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                                                                                                                             ; Sequence 25526, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                                                                APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblaen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25526
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Best Local Similarity 64.7%;
Matches 55; Conservative
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Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                         RESULT 11
US-10-282-122A-25526
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APPLICANT:
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US-10-123-155-480
; Sequence 480, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:

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456 SLYKEELEPKMPTPEKLMDWMMRMPEQRRGRECIIPDVSRSYHFGIVGLNMNGYFHEA 515
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333 ONLCIO
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT PILING DATE: 2002-04-15
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 480
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Gurney, Austin L.
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ORGANISM: Homo Sapien
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456 SLYKEELEPKWPTPEKLWDWDMWRMPEQRRGRECIIPDVSRSYHFGIVGLNMNGYFHEA 515
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                                                                                                                 516 YFKKHKFNTVPGVQLRNVDSLKKEAYBVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTY
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
593 TAGTCACGTTAATCTTTGAAAATAACGATGTAAAAGGTGCCGTTACGGGCGATGGCAAAA
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Best Local Similarity 8.5%; Pred. No. 1;
Matches 53; Conservative 193; Mismatches 372;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 480, Application US/10140472
Publication No. US20030138888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                  773 AACGIGCGTIGIACAAAATA 793
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Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
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Smith, Victoria
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
                 773 AACGIGCGIIGIACAAAAIA 793
                                                    636 PPSVTPIFLEPPPKEEGAPGA 656
                                                                                                                                                             Sequence 480, Application US/10146731
Publication No. US20030129692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stewart, Timothy A.
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Wood, William
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Beresini, Maureen
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Gurney, Austin L.
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ORGANISM: Homo Sapien
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                                                                              336 FIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTATFNLFPEAKFAVVLEED 395
                                                                                                               533 CAGCACGCGAAGCACAGCGCATGGGTGTAAAATTTGTTACTGGCACCCCGCAGGGTCGTG 592
                                                                                                                                         396 LDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMFGLGWVLRR 455
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                                                473 AAGGGTACTTTGCGCGTTCCGGCGCTGGCTGGGCACATGCAAGGAATGCCTTAGTGGCAG 532
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
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                                                                                                                                                                                                                                                                                                                                                                               773 AACGIGCGITGIACAAAAIA 793
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Stewart, Timothy A.
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Wood, William
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DeForge, Laura
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local S
Matches 53
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APPLICANT:
APPLICANT:
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219 PVFGEKHSKSPALSSWGDPVILKTDVPLSSAEEAECHWADTELNRRRRRFCSKVEGYGSV 278
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99 LDVEVYSSRSKVYVAVDGTTVLEDEAREQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDE 158
                                                                                                                                                                                                                                                                                              CGGAGCAATTTCGTAAACTGGCCCCGGAAGGCGTGTTGCAAGGTGATTTTCCGGGTTGGA 472
                                                                                                                                                                                                                                                                                                                                                                                                                 473 AAGGGTACTTTGCGCGTTCCGGCGCTGGCTGGGCACATGCAAGGAATGCCTTAGTGGCAG 532
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                                                                                                 516 YFKKHKFNTVPGVQLRNVDSLKKBAYEVEVHRLLSBAEVLDHSKNPCEDSFLPDTEGHTY
                                                         353 ATCGCCTGGGCGTCCGGGTACGTCCGGCCGAGATCCTAATCTGGTGGAACTTACCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 FIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTATFNLFPEAKFAVVLEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 CAGCACGCGAAGCACAGGCGCATGGGTGTAAATTTGTTACTGGCACCCCGCAGGGTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 TAGTCACGTTAATCTTTGAAAATAACGATGTAAAAGGTGCCGTTACGGGCGATGGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 SLYKEELEPKWPTPEKLWDWDMWRRMPEQRRGRECIIPDVSRSYHFGIVGLNMNGYFHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653 TTTGGAGAGGGGAACGTACATTCCTGTGTGCTGGGGCTAGCGCGGGTCAGTTCCTAGATT
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Job time : 923 secs
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US-09-031-059-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                US-09-031-059-2
                   Query Match
Sequence 2, Appli
Sequence 1623, A
Sequence 16923, A
Sequence 5414, Ap
Sequence 7672, Ap
Sequence 7672, Ap
Sequence 7897, Ap
Sequence 7897, Ap
Sequence 1624, A
Sequence 1444, Ap
Sequence 2, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Appli
Sequence 1, Appli
Sequence 5719, Ap
Sequence 962, App
Sequence 961, App
Sequence 961, App
Sequence 8104, App
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9143, Ap
Sequence 8941, Ap
Sequence 1, Appli
Sequence 1, Appli
                                                             // Search time 267 Seconds
(without alignments)
8696.167 Million cell updates/sec
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                                                                                                                        1 atgggaggttcggggtgacga......atcaccatcatcatcattaa 1419
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                                                                                                                                                                                                                                                                                      1: /cgn2 6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/RDTUS_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-232-463-14
US-09-902-540-165923
US-09-902-540-1263
US-09-902-540-1263
US-09-252-991A-7672
US-09-252-991A-7592
US-09-252-991A-7592
US-09-252-991A-7592
US-09-362-016-14624
US-09-313-294A-4144
US-09-313-294A-4144
US-09-103-840A-2
US-09-103-840A-1
US-09-103-840A-1
US-08-445-186-1
US-08-446-549-1
US-08-446-549-1
US-08-446-549-1
US-09-489-035A-5719
US-09-489-035A-5719
US-09-489-034A-5719
US-09-489-034A-961
US-09-101-464A-961
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US-09-103-840A-1
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Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                               May 29, 2005, 19:56:49
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                                                                                                                                                                                                           length: 0
length: 2000000000
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1419
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No.
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Sequence 282, App
Sequence 31175, A
Sequence 332, App
Sequence 312, App
Sequence 6724, Ap
Sequence 16509, Ap
Sequence 16509, Ap
Sequence 261, App
Sequence 17202, Ap
Sequence 1781, Ap
Sequence 1843, Ap
Sequence 1843, Ap
Sequence 1684, Ap
                                                                                                                                                                                                                                                                                           Sequence 14684, A
Sequence 11776, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KATO, NOBUO
APPLICANT: SAKAI, YASUYOSHI
APPLICANT: SAKAI, YASUYOSHI
APPLICANT: TANI, YOSHIKI
APPLICANT: TWOI, YOSHIKI
TITLE OF INVENTION: RECOMBINANT FRUCTOSYL AMINO ACID
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READ-0747
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,059
                                  US-09-313-294A-3938
US-09-25A-991A-392
US-09-25A-991A-9809
US-09-489-016-16509
US-09-949-016-16509
US-09-107-532A-261
US-09-902-540-4084
US-09-902-540-4084
US-09-902-540-4084
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US-09-902-540-4084
US-09-902-540-4084
US-09-902-540-4084
US-09-902-540-4084
US-09-949-016-11843
US-09-949-016-11843
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US-09-949-016-11843
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ATTORNEY FAGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REPERBENCE/DOCKET NUMBER: 0020-4253P
TELECOMMINICATION INFORMATION:
TELEPAN: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/899,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09031059
; Patent No. 5948659
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 2230
60424
3108
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3108
174
1200
1340
1344
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1187
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1189
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STRANDEDNESS: double
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1022 ATCGCGAGTTTATCATTGACCGTCATCCCGAATACCCGTCGCTTGTTCTTGGGTGTGGTG 1081
                                                                                                                                                                                                                                 1142 aggacaaaaccccggcaaaaarccacaaggcrgarccgcrggagcccggaaarcgcgarca 1201
                                                                                                                                                                                                                                                                                                                                                     1202 ACCGTAACTGGGGGGACAGATTAGGTCGATTTGGAGGGCCCAACCGGGTCATGGATTTCA 1261
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                                                                                           1118 CGAGCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGACGCGATGG
                                                                                                                                                                             1178 AAGGTAAAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGA
                                                                                                                                                                                                                                                                                              1238 ACCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGATGGATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                               1298 ATGATGTGAAGGAATGGACCAATGTTCAGTATCGTGATATTTCCAAGCT 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                1262 ATGAAGTGAAGGAGTGGACTAATGTCACCCAAAGGGACATCTCGGAAGTT 1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
18-08-32-463-14/c
18-quence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1800 Diagonal Road, CITY: Alexandria
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)836-9300
(703)683-4109
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pTZgpt-F1s
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GENERAL INPORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PLILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1263
LENGTH: 34953
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APPLICANT: Slater, Steven C.
APPLICANT: Missand, Roger C.
TITLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
FILE REFERENCE: 30-10(15849)B
CURRENT PELLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5414
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Pred. No. 0.97;
0; Mismatches 111; Indels
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Best Local Similarity 47.6%;
Matches 101; Conservative
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US-09-902-540-5414
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ORGANISM: Myxococcus xanthus
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Patent No. 6812339

GENERAL INCORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: RESELECTION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: RESELECTION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012
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  GCTGGCAGACCGTCCATTCAGCTTCGCACGCATTTGCTGGTGTGCCGAATACCGCGAATCG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                              942 CCAGATTCCAAAAGAAGCCGAAACGCGCGTTCGGGCCCTGCTGAAAGAGACAATGCCCCA 1001
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                                                                            GTTTTTCTTTGAACCCGATGAGGAGCGCGGTGAGATTAAAATATGCGATGAACACCCGGG 881
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US-09-902-540-5414
; Sequence 5414, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
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Best Local Similarity
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US-09-949-016-16923
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ORGANISM: Human
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LENGTH: 390416
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794 CCACCACCGCCAGGAGGATTACCGCACTGTCCACCCAGAAGCCGAGCAGCGGGGGGTGA 738
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7592
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Patent No. 6551795
GENERAL INFORMATION:
APPLICAMTS MATC J. Rubenfield et al.
APPLICAMTS MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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1 Similarity 55.6%; Pred. No. 0.74;
65; Conservative 0; Mismatches 52; Indels
                                                         27185 GÉTÉACCÉCÉCETTCAACGACCTÉCÉCECE 27216
                     408 CCGCCCGGAGCAATTTCGTAAACTGGCCCCGG
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ORGANISM: Pseudomonas aeruginosa
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Matches 65; Conserv
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Matches 65; Conserv
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US-09-252-991A-7887/c
                                                                                                                                    US-09-252-991A-7672
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US-09-22-991A-7592

Sequence 7592, Application US/09252991A

Factor No. Application US/09252991A

Patent No. 6551795

GENERAL INPORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 2739
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; Sequence 7958, Application US/09252991A
; Sequence 7958, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
    APPLICANT: Maxc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFREENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR PILING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7958
; LENGTH: 2778
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2.4%; Score 33.8; DB
Best Local Similarity 55.6%; Pred. No. 2.8;
Matches 65; Conservative 0; Mismatches
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2.4%; Score 33.8; DE
Best Local Similarity 55.6%; Pred. No. 2.8;
Matches 65; Conservative 0; Mismatches
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TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
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VS-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
                                                                                                                                                                                                                                           134 CCGTGCTG 141
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US-09-103-840A-2/c
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                                                                                                     GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-10-03
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Sequence 4144, Application US/09313294A

Sequence 4145, Application US/09313294A

Sequence 4146, Application US/09313294A

SEQUENCE No. 4076212

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US

CURRENT PLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 ACCCGCCCGGAGCAATTTCGTAAACTGGCCCCGGAAGGCGTGTTGCAAGGTGATTTTCCG 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%; Score 33.8; DB 4; Length 1: Best Local Similarity 52.5%; Pred. No. 53; Matches 74; Conservative 0; Mismatches 67; Indels
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; OTHER INFORMATION: Incyte ID No. 6476212 700347784H1
US-09-313-294A-4144
                                                  Sequence 14624, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48053 GCTGCAGAGAGGAGAAGGA 48073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 GTGGCAGCACCACGCAAGCA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(147382)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
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                         US-09-949-016-14624
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LENGTH: 281
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835772 CCGAGCAGCAGCCCCCCGGCGCCGCTACCACCGACACCCGGCGGGACCCCAAGCCCG
                                                                                                             246 grgaaccagcagargccrcrgccgargccaraggrcarcarccrccrcgcrgrcrgsag 187
                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Clair M.
APPLICANT: PRASER, Clair M.
APPLICANT: PRASER, Clair M.
APPLICANT: PRASER, Clair M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHANN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: PEASER, Claire M.
APPLICANT: PEASER, Claire M.
APPLICANT: PEASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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NUMBER OF SEQ ID NOS:
SEQ ID NO 8941
LENGTH: 1818
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US-09-252-991A-9143/C
; Sequence 9143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc. J. Rubenfield et al.
; APPLICANT: Marc. J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
; FILE REPERERRICE: 107196.136
; FILE REPERERRICE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR PLING DATE: 1998-02-18
; PRIOR PLING DATE: 1998-02-18
; PRIOR PLING DATE: 1998-02-18
; RIOR APPLICATION NUMBER: US 60/094,190
; RIOR APPLICATION NUMBER: US 60/094,190
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; RIOR APPLICATION NUMBER: US 60/094,190
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                      833594 CCGAGCAGCCCCCCCGGCCCCCCGTACCACCGACACCCGGCGGAACCCCAAGCCCG
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                                                                                                                                                                  95 CGGCTCTGCACCTCGCGCGCGCGGGATATACCAACGTTACCGTGCTGGACCCCTATCCTG 154
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48.2%; Pred. No. 1.5;
Live 0; Mismatches 101; Indels
                                                    Query Match 2.4%; Score 33.6; DB 3; Length 4 Best Local Similarity 59.4%; Pred. No. 2.9e+02; Matches 57; Conservative 0; Mismatches 39; Indele
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US-09-252-991A-8941
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  US-09-103-840A-1
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Best Local S
Matches 94
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0
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Job time : 277 secs
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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33142
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM nucleic - nucleic search, using sw model

May 29, 2005, 19:23:28 ; Search time 6433 Seconds (without alignments) 10688.318 Million cell updates/sec Run on:

US-10-622-893A-6 1419 Perfect score: Title:

Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4708233 seqs, 24227607955 residues Searched:

9416466

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

90 ba ... 90 ba gb_sy:* gb_un:* gb_vi:* GenEmbl:* 101 **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•		d)	
Result		Query				
No.	Score	Match	Match Length DB	DB	σī	Description
7	846.4	59.6	1559	8	AFU82830	U82830 Aspergillus
7	685	48.3	1314	9	AR072866	AR072866 Sequence
m	685	48.3	1314	9	E14942	E14942 Asperdillus
4	685	48.3	1314	ø	E14955	E14955 Aspergillus
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9	685	48.3	1314	8	ATFAOA	Y09020 A.terreus m
7	657.6	46.3	1311	8	AB180733	AB180733 Aspergill
80	354.8	25.0	1526	œ	AF035700	AF035700 Aspergill
6	350.4	24.7	1338	8	AB180732	AB180732 Aspergill
10	335.2	23.6	1320	9	BD173827	BD173827 Compositi
11	335.2	23.6	1320	9	E16562	E16562 Fusarium ox
12	333.6	23.5	1320	9	BD173829	BD173829 Compositi
13	332	23.4	1320	9	BD173828	BD173828 Compositi
14	332	23.4	1320	9	BD173830	BD173830 Compositi
c 15	127	8.9	110000	8	CR382133_02	Continuation (3 of
16	62.8	4.4	1314	9	AX712067	AX712067 Sequence
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18	61.2	4.3	77986	æ	BX897677	BX897677 Neurospor
19	57.6	4.1	1314	9	E22308	E22308 DNA encodin

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Arugzejo 1559 bp mRNA linear PLN 15-MAY-1997
Aspergillus fumigatus fructosyl amine: oxygen oxidoreductase mRNA,
complete cds.
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1559)
Takahashi, M., Pischetsrieder, M. and Monnier, V. M.
Molecular cloning and expression of amadoriase isoenzyme (fructosylamine:oxygen oxidoreductase, EC 1.5.3) from Aspergillus fumigatus
J. Biol. Chem. 272 (19), 12505-12507 (1997)
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Takahashi,M., Pischetsrieder,M. and Monnier,V.M.
Takahashi,M., Pischetsrieder,M. and Monnier,V.M.
Direct Submission
Submitted (20-DEC-1996) Pathology, Case Western Reserve University,
2085 Adelbert Rd., Cleveland, OH 44106, USA
Location/Qualifiers
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/organism="Aspergillus fumigatus"
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Aspergillus terreus mRNA for fructosyl amino acid oxydase (FAOD-L). E14942

RESULT 3 E14942 LOCUS DEFINITION ACCESSION VERSION

JP 1998033177-A/1.
Aspergillus terreus
Aspergillus terreus
Bukeryota; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1314) 217 124 184 277 244 304 397 364 517 ATGCCTTAGTGGCAGCAGCACGCGAAGGGCATGGGGTGTAAATTTGTTACTGGCA 577 CTCTGCACCTCGCGCGCGCGCGGGATATACCAACGTTACCGTGCACCCCTATCCTGTCC 157 398 TGGAACTTACCCGCCCCGCAGCAATTTCGTAAACTGGCCCCGGAAGGCGTGTTGCAAGGTG 457 365 CCGAATTGACTCGGCCGGAGCAGTTCCGCCAGCTGGCCCCC---GGCGTCTTGAAGGGTA 421 Actrococcinicales de de la contra del la contra della con PN JP 1998033177-A/1
PD 10-PEB-1998
P 23-JUL-1996 JP 1996193344
PI KATO NOBUO, SAKAI YASUYOSHI, TANI YOSHIKI, FUKUYA HIROSHI PC C12N15/09, C07H21/04, C12N1/21, C12N9/06, C12P21/02, C12Q1/26, PC 64 245 AAAATGACCCCATCTTCAAGCCGTACTACCACGACACGCGCGTCGTGATGTCCGCCACCA carcadecarrredecedeceaceaceacaacaacaacarcarcerecedecagracaeca CGCAGGAGGGCCTGGATCGCCTGGGCGTCCGGGTACGTCCGGGCGAGGATCCTAATCTGG cadricaccaagrichricgricanantigaricandeseseseseseseneseseneseneses 158 CTAGCGCCATCTCCGCCGGAAACGACGTGAAGAAGTCATTAGCAGTGGCCAATATTCGA 218 ATAACAAAGACGAAATCGAAGTGAATGAGATCTTGGCGGAAGAGGCGTTTAACGGTTGGA GCAAGAAGGACGACGACGAAGTCAATGAGATTATCGCCGAACAGGCCTTCAATGGCTGGA 38 CCGTCACTAAGTCATCATCTCTCCTGATCGTTGGTGCCGGGACTTGGGGCACCTCAACGG ATTITCCGGGTTGGAAAGGGTACTTTGCGCGTTCCGGCGCTGGGCTGGGCACATGCAAGGA Gaps oxydase, 3; FT Length 1314; /organism='Aspergillus terreus' acid h Similarity 70.7%; Score 685; DB 6; Length 13 Similarity 70.7%; Pred. No. 5.7e-192; 26; Conservative 0; Mismatches 380; Indels 1314
 product='fructosyl amino Kato, N., Sakai, Y., Tani, Y. and Fukuya, H. FRUCTOSYL AMINO ACID OXIDASE Patent: JP 1998033177-A 1 10-FEB-1998; KDK CORP 1314
 /organism="Aspergillus terreus" /mol_type="genomic DNA"
 /db_xref="taxon:33178" Location/Qualifiers Ci2R1:19), (C12N9/06, C12R1:19); strandedness: Double; clone='pFAL2 .1314 Location/Qualifiers terreus Aspergillus terrer JP 1998033177-A/1 10-FEB-1998 topology: Linear; /strain='GP1' Query Match Best Local Similarity 70.7° Matches 926; Conservative (C12N1/21, PC C12R1 CC stran CC topol FH Key FH SOURC 458 422 518 ò 요 8

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Kato,N., Sakai,Y., Tani,Y. and Fukuya,H.
RECOMBINED FRUCYOSYL AMINO ACID OXIDASE
Patent: JP 1998033180-A 1 10-FEB-1998;
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                                        FUKUYA HIROSHI
C1201/26, PC
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PD 10-FEB-1998

PF 24-JUL-1996 JP 1996194557

PI KATO NOBUO, SAKAI YASUYOSHI, TANI YOSHIKI, FUKUYA HIROS C12N15/09, C07H21/04, C12N1/19, C12N9/06, C12P21/02, C12Q1/26, PC G01N33/66, (C12N1/19, C12R1:72), (C12N9/06, C12R1:72); CC strandedness: Double; CC topology: Linear; EH Key

FH Key

RT source

1. .1314

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KATO NOBUO, SAKAI YASUYOSHI, TANI YOSHIKI, FUKUYA HIR
5/09,C07H21/04,C12N1/19,C12N9/06,C12P21/02,C12Q1/26,
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Pred. No. 5.7e-192;
                                                                                                                                                                                                                                                                     1. .1314
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                                                                                                                                                                                                                                                                                                                                        1. .1314
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/mol_type="genomic DNA"
/db_xref="teaxon:33178"
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                                                                                                                                                                                                                                             48.3%; Score 685; DB 6; Length 13 70.7%; Pred. No. 5.7e-192; ative 0; Mismatches 380; Indels
                                        1. .1314
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   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Conservative
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(C12N1/21,C12R1:19),(C12N9/06,C12R1:19),C12N15/00,(C12N15/00,C12R1:66)
Strandedness: Double,
Topology: Linear;
                                                                 CGTTAAAACCGGAAGAACGTGCGTTGTACAAAAATATACCGGTTATCTTTAACATCGAAC
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/organism='Aspergillus terreus GP1'.
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Yoshiki,T., Tori.K., Nobuyuki,Y., Akio,K. and Hiroshi,F.
Thermostable fructosylamino-acid oxidase
Patent: JP 1999221081-A 1 17-AUG-1999;
KYOTO DAILCHI KAGAKU CO LTD
OS ARPEYGILUS terreus GP1
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RWSPEIAINRNWGDRLGRFGGPNRVMDFNEVREWTNVTQRDISKL"
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                                                                                                                     3,
                                                                                     Length 1314;
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Pred. No. 5.7e-192;
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Best Local Similarity 70.7%;
Matches 926; Conservative
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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Submitted (23-OCT-1996) N. Kato, Fac. of Agriculture, Kyoto Univ.,
Kitashirakawa-oiwake-cho, Sakyo-ku, Kyoto 606-01, JAPAN
Location/Qualifiers
                                                                                                                                                                       CGAGCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primary structures of fungal fructosyl amino acid oxidases and their application to the measurement of glycated proteins Eur. J. Biochem. 242 (3), 499-505 (1996)
                                                                                                       ATCGCGAATTCCTGATAGATCGACATCCGCAGTACCACAGTCTTGTGTTGGGCTGTGGTG
                                  CCCAGCTGGCAGACCGTCCATTCAGCTTCGCACGCATTTGCTGGTGTGCCGATACCGCGA
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facA gene, flavoprotein, fructosyl amino acid oxidase.
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/mol type="mRNA"
/isolate="GP1"
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NALVAAIREAEKLGVKFVTGTQGRVITLIFENNDVKGAVTADGKIWRAEGTVLCAGAN
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DEHFGYTNWYKSADGHLTSLPFEKTQIPKESEARVRALLSETWPQLADRPFSFARVCW
CADTANREFIIDKHPEERPSLVLGCGASGRGFKYLPSIGNLIVDAIBDKVPEKVHKLTR
WSPDIAVDRKWRDTLGRFGGPNRVMDFHDVKEWTNVQNKDTAKL"
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                                                                                                                        CTTCAGGACGAGGCTTCAAATATCTTCCCTCGATCGGAAGCATCGTCGCAGAGCGATCGCATGG 1141
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Akazwa, S., Karino, T., Yoshida, N., Katsuragi, T. and Tani, Y. Direct Submission

Biblitted (29-MAY-2004) Shin-ichi Akazawa, Graduate School of
Biblogical Sciences, Nara Institute of Science and Technology;
8916-5 Takayama, Ikoma, Nara 630-0192, Japan
(E-mail:s-akazaw@bs.aist-nara.ac.jp, Tel:81-743-72-5423,
Location/Qualifiers
                                                     ATCGCGAATTCCTGATAGATCGACATCCGCAGTACCACAGTCTTGTGTTGGGCTGTGGTG
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/product="fructosyl-amino acid oxidase"
/protein id="BAD54825."
/db_xref="G1:53850452"
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/mol_type="mRNA"
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Score 657.6; DB 8;
Pred. No. 8.1e-184;
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11 CGCCGGAAAGACGCATGAACGCCCCCCCCCATCCAGTCCCTCAACCCCCTTTACCAGTCCCTCCC	CCGTGCTTTCTTGATCGATCTGAACACCCCTCACTGCTGGGGGGGG
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GWHIAKKANFSARRKGYTFITGSPEGDVVSLIYENGDVVGARTAADGTWHRADHT
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PLSPARICMDADTVDRAFLIDRHPEYRSLLLAVGGSGNGAMQMPTIGGFIADALBGNL
QKELKHALRWRPEIAAQRDWKDTQNRFGGPNKVMDFQKVGENEWTKIGDKSRL"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                      TCGAGATTGGAGAGCGACTCAGAATCGCTTTGGCGGGCCTGACAGGATCATGGATTTTCA
                                   CCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGTGATGGATTTTTCA
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Submitted (29-MAY-2004) Shin-ichi Akazawa, Graduate School of
Biological Sciences, Nara Institute of Science and Technology,
8916-5 Takayama, Ikoma, Nara 630-0192, Japan
(E-mail:8-akazaw@bs.alst-nara.ac.jp, Tel:81-743-72-5423,
Pax:81-743-72-5429)
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/product="fructosyl-amino acid oxidase"
/protein_id="RAD54624.1"
/db_xref="GI:53850450"
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/db_xref="taxon:5062"
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Best Local Similarity 55.9%;
Matches 713; Conservative
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UP 1998201473-A/1.
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1217 TTGCCGCCCAACGAGCTGGAAGGATACGCAAAATAGATTCGGAGGTCCGAATAAAGTAA 1276
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Kozuma, T., Yoshioka, I., Arai, M., Sumitani, J. and Imamu, S.
Compositions for assaying alycoprotein
Patent: WO 02061119-A 1 08-AUG-2002,
ASAHI KASEI CORP.TAKUJI KOZUMA, ISSEI YOSHIOKA, MOTOO ARAI, JUNICHI
SUMITANI, SHIGEVICKI INAMURA
OS FUBATIUM OXYSDORUM IFO-9722
PN WO 02061119-A/I
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                                                                                                                       TTGCGTTAAAACCGGAAGAACGTGCGTTGTACAAAAATATACCGGGTTATCTTTAACATCG
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I (bases 1 to 1320)
S (Nozuma,T., Yoshioka,I., Arai,M., Sumitani,J. and Imamu,S. Compositions for assaying glycoprotein
Patent: WO 02061119-A 3 08-AUG-2002;
ASAMI KASHI CORP. TAKUJI KOZUMA, ISSEI YOSHIOKA, MOTOO ARAI, JUN SUMITANI, SHIGEYUKI IMAMURA
OS Artificial Sequence
PN WO 02061119-A/3
PP 30-JAN-2002
PP 30-JAN-2002
PP 30-JAN-2001
PP 240002
PP 31-JAN-2001 JP 01P 022953, 16-FEB-2001 JP 01P 039796
08-AUG-2001 JP 01P 240002
PI TAKUJI KOZUMA, ISSEI YOSHIOKA, MOTOO ARAI, JUNICHI SUMITANI SHIGEYUKI IMAMURA
PC C12Q1/26, C12Q1/37, C12N15/09, G01N33/68, G01N33/72 CC
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                                                                                                                   20-JAN-1997 JP 1997007101
SHIMIZU AKIRA, KOGA SHINJI
C12N15/09,C12N1/21,C12N9/06//C12Q1/26,(C12N1/21,C12R1:19),
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                     PURE
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 Shimizu, A. and Koga, S. PRUCTOYL SUBSTANTIALLY PRUCTOSYL ANINE OXIDASE-PRODUCTIVE SUBSTANTIALLY Parent: JP 1998201473-A 1 04-AUG-1998; ASAHI CHEM IND CO LTD
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llarity 55.3%; Pred. No. 7.2e-88;
Conservative 0; Mismatches 568;
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topology: Linear;
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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PN WO 02061119-A/2
PD 08-AUG-2002
PP 08-AUG-2002
PF 30-JAN-2001 JP 01P 022953,16-FEB-2001 JP 01P 039796 PR
11-JAN-2001 JP 01P 022953,16-FEB-2001 JP 01P 039796 PR
08-AUG-2001 JP 01P 240002
PT TAKUJI KOZUMA,1SSEI YOSHIOKA,MOTOO ARAI,JUNICHI SUMITANI, PI
SHIGEYUKI IMAMURA
PC C12Q1/26,C12Q1/37,C12N15/09,G01N33/68,G01N33/72 CC
Compositions for assaying glycoprotein
FH Key Location/Qualifiers
FT CDS (11. (1320)
FT mutation (1114). (1115).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1211 TTACCGAGTTCTGGGGTAAAGATCCTCTGGATCGGTTTGGAGCTGACGATAAGATCATGG
     851 ATCCGGGCTACTGCAACTGGGTTGAAAAGCCTGGTTCTAAGTACCCCCCAGTCCATCCCCT
                                                                                                                                                           1052 CCGCGAATCGCGAATTCCTGATAGATCGACATCCGCAGTACCACAGTCTTGTGTTTGGGCT
                                                                                                                                                                                                                                                                                                          1031 CACAGGATAGAATGTTCCTGATCACCTATCATCCTCGACATCCCTCACTTGTT
                                                                                                                                                                                                                                                                                                                                                                  1112 GTGGTGCGAAGAGGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1232 CGGCGAACCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGTGATGG
                                                        TCGAAAAAACCCAGATTCCAAAAGAAGCCGAAAACGCGCGTTCGGGCCCTGCTGAAAGAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences.

(bases 1 to 1320)

Kozuma,T., Yoshioka,I., Arai,M., Sumitani,J. and Imamu,S.

Compositions for assaying glycoprotein

Patent: WO 02061119-A 2 08-AUG-2002;

ASAHI KASEI CORP,TAKUJI KOZUMA,ISSEI YOSHIOKA,MOTOO ARAI,

SUMITANI, SHIGEYUKI IMAMURA

OS Artificial Sequence

PN WO 02061119-A/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1271 ATTTGCCCAAGAGTGATGTAGAGGGATGGACAAATATCAAGAAT 1314
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Compositions for assaying glycoprotein.
BD173828
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(1114). .(1115)
Location/Qualifiers

    1320
    /organism="synthetic compositype="genomic DNA"
    /db_xref="taxon:32630"

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synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCACCTCGCGCGCCGCGGATATACCAACGTTACCGTGCTGGACCCCTATCCTGTCCCTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 CACCGATATCAGCCGGGCATGATGTAAACAAACTTGCTGGCCGACTGTCGACTGCCGATA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GCAAAGGTGATGATGAAGACTCAATCTGGAAAGCACTTAGCTACGCCGCAGCTCAAGGAT 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 GTAACTTTCCAGGCTGGAAGGGCTTTTACAAGCCCACGGGTTCTGGTTGGGTTCATGCTC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 GCTCTCCCGAAGGAAAGGTGGAGAGTCTGATCTTTGAAGACGCCGATGTTCGAGGTGCCA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 AGACGCAGATGGTAAGGAGCACAGAGCGGATCGAACTATTCTTTCCGCTGGTGCTTCAG 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCGGGCTACACAAATATGGTCCAGAGTGCAGACGCCACG---ATGATGAGCATTCCGT 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 ATACACCTCTCAACACAGAGAAGATTTCAGAAAGACCATGCCTGAGGGTATCCTGACAG
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                                                                                                                                                                                                                                                                                          Length 1320;
                                                                                                                                                                                                                                                                                       Score 333.6; DB 6; Length
Pred. No. 2.1e-87;
0; Mismatches 569; Indels
Compositions for assaying glycoprotein FH Key Location/Qualifiers FT CDS (1). (1320) FT mutation (1115).
                                                                                                   Location/Qualifiers
1. 1320
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                       Query Match 23.5%;
Best Local Similarity 55.2%;
Matches 720; Conservative
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PR 31-JAN-2001 JP 01P 022953,16-FEB-2001 JP 01P 0.5...
PR 31-JAN-2001 JP 01P 240002
PR 31-JAN-2001 JP 01P 240002
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PC C12Q1/26,C12Q1/37,C12N15/09,G01N33/68,G01N33/72 CC
COmpositions for assaying 91ycoprotein
FH Key Location/Qualifiers
FT CDS (1) (1320)
FT mutation (1114). (1115).
Location/Qualifiers

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions for assaying glycoprotein
Patent: WO 02061119-A 4 08-AUG-2002;
ASAHI KASZEI CORP, TAKUJI KOZUMA, ISSEI YOSHIOKA, MOTOO ARAI, JUNICHI SUMITANI, SHIGSYUKI IMMURA
OS Artificial Sequence
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                           CGATGGAAGGTAAAAGTGCCGCAAAAAATTCACGAATTAATCAAGTGGAACCCCGGACATTG
                                                                       1151 GTATGGAGGGTACGCTTGAGGAAAGGTTTGCCAAGTTCTGGAGATGGCGACCAGAGAAGT
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Kozuma,T., Yoshioka,I., Arai,M., Sumitani,J. and Imamu,S.
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TCACCAAACAGTCCCAAATTCTCATCGTTGGTGGCGGAACTTGGGGATGCTCAACTGCCC 70
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                             311 CAACACCAAAGTCTATCAAGCAGCTGGTAGAAGATGAGATCGGTGACGACATCGACCAGT
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Scoring table: Sequence:

4390206 seqs, 2959870667 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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		Description	Aav09626 A. terreu	Aaz07721 Heat-resi	Aav00732 Aspergill	Aav44893 Fructosyl	Abk90475 Fusarium	Abk90477 Fusarium	Abk90476 Fusarium	Abk90478 Fusarium	Adm78788 Fusarium	Ads15772 Fructosyl	Ade81212 Orf20 cod	Ade81173 ML-236B s	Acc48873 Eupenicil	Aax15949 DNA encod	Aat85703 Coding se	Aax15950 DNA encod	Acc48872 Coniochae	Adm78786 Fusarium	Ada71938 Rice gene	Ado39657 Aspergill
SUMMARIES		Ð	AAV09626	AAZ07721	AAV00732	AAV44893	ABK90475	ABK90477	ABK90476	ABK90478	ADM78788	ADS15772	ADE81212	ADE81173	ACC48873	AAX15949	AAT85703	AAX15950	ACC48872	ADM78786	ADA71938	AD039657
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	Query	Match	48.3	48.3	48.2	23.6	23.6	23.5	23.4	23.4	22.9	8.1	5.5	5.5	4.4	4.1	3.8	3.8	3.6	3.3	3.2	2.7
		Score	685	685	683.4	335.2	335.2	333.6	332	332	324.4	115.2	78.6	78.6	62.8	57.6	53.6	53.6	50.4	46.4	44.8	38.8
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ALIGNMENTS

Fructosylamino acid oxidase; FAOD-L; Amadori compound; ds. AAV09626 standard; cDNA to mRNA; 1314 BP (KYOT-) KYOTO DAIICHI KAGAKU KK. 96JP-00194557. 96JP-00194557. (first entry) A. terreus FAOD-L CDNA. Aspergillus terreus. WPI; 1998-172097/16. P-PSDB; AAW39253. JP10033180-A. 24-JUL-1996; 14-MAY-1998 24-JUL-1996; 10-FEB-1998. AAV09626;

Aspergillus terreus recombinant fructosyl:amino acid oxidase - used for analysis of "Amadori" compound(s).

Example 1; Col 23-26; 18pp; Japanese.

This sequence encodes a novel recombinant fructosylamino acid oxidase (FAOD-L) produced from enkaryotic cells integrated with an RT-FCR product encoding FAOD-L derived from Aspergillus terreus GP1 (FERM P-15664). FAOD-L can be used for the analysis of "Amadori" compounds

Sequence 1314 BP; 294 A; 371 C; 395 G; 254 T; 0 U; 0 Other;

ä Gaps 3, Query Match
48.3%; Score 685; DB 2; Length 1314;
Best Local Similarity 70.7%; Pred. No. 2.5e-218;
Matches 926; Conservative 0; Mismatches 380; Indels 3

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CTTCAGGACGAGGCTTCAAATATCTTCCCTCGATCGGAAGCATCATCGCAGACGCCATGG
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                                                                            1142 Aggacadadaccicogcadadarcoacadocroarcogcrosoagecocogadaroacad
                                                                                                                1238 ACCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGGTCCAAATCGTGTGATGGATTTTTC
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1. .1314
/*tag= a /product= "fructosyl amino acid oxidase (FAOD)"
                                                                                                                                                                             ATGATGTGAAGGAATGGACCAATGTTCAGTATCGTGATATTTCCAAGCT 1346
                                                                                                                                                                                              Length 1314;
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Matches 926; Conservative
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This cDNA sequence comprises a coding region for an Aspergillus terreus fructosyl amino acid oxidase (FAAO, see AAW3141), designated FAOD-L, that shows higher FAAO activity on fructosyl lysine than on fructosyl value. Total RNA of a terreus GPI was subjected to PCR using primers (see AAV00733-34) based on the partial amino acid sequence of native FAOD-L. The resulting 400 bp PCR fragment was used to screen an A. terreus CPI cDNA library. DNA excised from positive clones was used to transform plasmid pFAL2 that included the 1314 bp coding region. E. coli SOLR containing pFAL2 that included the 1314 bp coding region. E. coli SOLR containing pFAL2 was deposited as FERM BP-5981. The invention provides recombinant FAAO, DNA encoding the FAAO, an expression vector containing the DNA, a transformed by the vector, and a method of preparing recombinant FAAO by culturing the transforment. The FAAO can be used in assays for, e.g. determination of amadori compounds such as cultural, diagnosis and monitoring of diabetes or quality control of foods. (Updated on 17-OCT-2003 to standardise OS field)
                          ACCGTAACTGGCGTGATACTCTGGGGGCGTTTTGGCGGTCCAAATCGTGTGATGGATTTTC 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant fructosyl amino acid oxidase - useful in assays for amadori compounds, e.g. in diabetes diagnosis or food analysis.
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                                                                                                                                           Fructosyl amino acid oxidase; FAOD-L; amadori compound; assay; food analysis; diabetes; diagnosis; ds.
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                                                                                                             ATGATGTGAAGGAATGGACCAATGTTCAGTATCGTGATATTTCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus terreus; strain GP1 (FERM BP-5684)
                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                              to mRNA; 1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAIICHI KAGAKU CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 20-21; 33pp; English
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                                                                                                                                                                                                                                                                                                                         CGCAGGAGGCCTCGATCGCCTGGGCGTCCGGGTACGTCCGGGCGAGGATCTAATCTG 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTGCATCTTGCCCGCAGAGGATACACCAATGTCACTGTCCTTGACCCGTACCCGGTTC 124
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                                                                                                                                                    218 ATAACAAAGACGAAATCGAAGTGAATGAGATCTTGGCGGAAGAGGCGGTTTAACGGTTGGA
                                                                                                                                                                               185 GCAAGAAGGACGAGGTCGAAGTCAATGAGATTATCGCCGAACAGGCCTTCAATGGCTGGA
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1142 AGGACAAAACCCCGGCAAAATCCACAAGCTGATCCGCTGGAGCCCGGAAATCGCGATCA 1201 100 220 101 TGCACCTCGCGCGCGCGGGATATACCAACGTTACCGTGCTGGACCCCTATCCTGTCCTA 160 131 cacceararcaecedescareareraacaaacraecreecedaceacresceacreecedra 190 274 71 recarcitégecegrégégerracaccaacgreacritérreregargreaterecarecege 130 191 gcałakogronickiekancickarcickancickachinacikoccockacickackar 250 334 microbe with 70 GGAAGAACGACCCGCTTTTCAAACCGTATTATCATGATACGGGCCTGCTGATGTCTGCTT 1238 ACCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGTGATGGATTTTTC 41 TCACTAAGTCATCATCTCCTGATCGTTGGTGCCGGGACTTGGGGCACCTCAACGGCTC 161 GCGCCATCTCCGCCGGAAACGACGTGAACAAGTCATTAGCAGTGGCCAATATTCGAATA 221 ACAAA-----GACGAAATCGAAGTGAATGAGATCTTGGCGGAAGAGGCGTTTAACGGTT - used for producing fructosylamine This sequence encodes the fructosylamine oxidase produced by the of the invention. The microbe can produce fructosylamine oxidase 1298 ATGATGTGAAGGAATGGACCAATGTTCAGTATCGTGATATTTCCAAGCT 1346 1262 ATGAAGTGAAGGAGTGGACTAATGTCACCCAAAGGGACATCTCGAAGTT 1310 15; 'Match 23.6%; Score 335.2; DB 2; Length 1320; Local Similarity 55.3%; Pred. No. 7e-101; les 721; Conservative 0; Mismatches 568; Indels 15; Sequence 1320 BP; 348 A; 333 C; 330 G; 309 T; 0 U; 0 Other;

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ABK90475;
CAGGTGATTGCGGCACGGTTACAAGCATATCACATCAATTGGAAAGTTCATCTCTGACT 1150
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                           311 caacaccaaágrcrarcaagcagcrógragaagargagrcggrógacargaccágr 370
                                                                                                                    Graactriccaddcriddaaddccrittiacaadcccacccriccriccriccardcric 490
                                                                                                                                                                                                              GAAAAGCTATGAAAGCTGCTTTCGAAGAGAGAGAGACTTGGTGTCAAATTCATCACTG 550
                                                                                                                                                                                                                                             GCACCCCGCAGGGTCGTGTAGTCACGTTAATCTTTGAAAATAACGATGTAAAAGGTGCCG 634
                                                                                                                                                                                                                                                                           GCTCTCCCGAAGGAAAGGTGGAGAGTCTGATCTTTGAAGACGGCGATGTTCGAGGTGCCA 610
                                                                                                                                                                                                                                                                                                         CGGGTCAGTTCCTAGATTTCAAGAATCAACTTCGACCAACCGCTTGGACCCTGGTACACA 754
                                                                                                                                                                                                                                                                                                                                                                                                  CAGAGTICTICCTCGATTTTGAGAACCAGATCCAGCCTACGGCGTGGACCCTGGGCCATA 730
                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCGTTAAAACCGGAAGAACGTGCGTTGTACAAAATATACCGGTTATCTTTAACATCG 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                           rccagargacaccagaagaaaccaagcrigracaagaccrigccaccrcrrrrcaacarca 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        791 ACCAAGGTTTCTTCATGGAACCTGATGAGGATCTTCATCAACTCAAGATGTGCGATGAAC 850
GCTCGCAGGAGGGCCTGGATCGCCTGGGCGTCCGGGTACGTCCGGGCGAGGATCCTAATC 394
                                                                                                                                                                                                                                                                                                                              GGAATGCCTTAGTGGCAGCAGCACGCGAAGCACAGCGCCATGGGTGTAAAATTTGTTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 ATCCGGGCTACTGCAACTGGGTTGAAAAGCCTGGTTCTAAGTACCCCCAGTCCATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGGGGGTTTTTTTTGAACCCGATGAGGAGCGCGGTGAGATTAAAATATGCGATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAAAAAACCCCAGATTCCAAAAGAAGCCGAAACGCGCGTTCGGGCCCTGCTGAAAGAGA
                                                         TGGTGGAACTTACCCGCCCGGAGCAATTTCGTAAACTGGCCCCCGGAAGGCGTGTTGCAAG
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The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a concanavalin A and betaine and/or ascorbic oxidase and a buffer without a compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound proportion of albumin into glycoalbumin with respect to the other albumin measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and steabilise enzymes such as protease acting on glycoamino acids. This sequence represents DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω,
                                                                                                                               Glycoamino acid; glycoprotein; deoxycholic acid; deoxycholic amide; gene; cholic acid amide octyl glucoside; quaternary ammonium salt; ds; dsudeternary ammonium salt cationic surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes; ascorbic acid; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Fusarium oxysporum polypeptide #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1320 BP; 348 A; 333 C; 330 G; 309 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "No start or stop codon given"
/transl except= (pos:736. .738, aa:Ile)
/transl_except= (pos:1186. .1188, aa:Tyr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sumitani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis and management of diabetes.
                                                                   Fusarium oxysporum polynucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 63-65; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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16-FEB-2001; 2001JP-00039796
08-AUG-2001; 2001JP-00240002
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P-PSDB; ABG30782.
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16-FEB-2001; 2001JP-00039796.
08-AUG-2001; 2001JP-00240002.
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                                          71 TCCATCTCGCCCGTCGGGGTTACACCAACGTCACTGTTCTCGATGTCAATGCGCATCCGT 130
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TCACCAAACAGTCCCAAATTCTCATCGTTGGTGGCGGAACTTGGGGGATGCTCAACTGCCC
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                                                                GCGCCATCTCCGCCGGAAACGACGTGAACAAAGTCATTAGCAGTGGCCAATATTCGAATA
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1211 TTACCGAGTTCTGGGGTAAGATCCTCTGGATCGGTTTGGAGCTGACGATAAGATCATGG 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholic acid amide octyl glucoside; quaternary ammonium salt; ds; quaternary ammonium salt cationic surfactant; concanavalin A; betaine; ascorbic oxidase; 4-(2-hydroxyethyl)-1-piperazinyl group; albumin; protease; glycoalbumin; bromocresol purple; glycation; diabetes; ascorbic acid; mutant.
CGATGGAAGGTAAAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCCGGACATTG
                                                                        1151 GTATGGAGGGTACGCTTGAGGAAAGGTTTGCCAAGTTCTGGAGATGGCGACCAGAGAAGT
                                                                                                                                                             CGGCGAACCGTAACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGATGG
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                                                                                                                                                                                                                                                                                                                           ATTITC-----ATGATGTGAAGGAATGGACCAATGTTCAGTAT 1329
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/product= "Fusarium oxysporum polypeptide
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/transl_except= (pos:736. .738, aa:1le)
/transl_except= (pos:1186. .1188, aa:Tyr)
replace[115,A)
/*tag= b
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1172 CGATGGAAGGTAAAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTG 1231
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                                                                                                                                                                                                                                       GTGGTGCGAGCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGACG
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                                                              TCGAAAAAACCCAGATTCCAAAAGAAGCCGAAACGCGCGTTCGGGCCCTGCTGAAAGAA
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(pos:736. .738, aa:11e)
(pos:1114. .1116, aa:Trp)
(pos:1186. .1188, aa:Tyr)
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                                   ACCCGGCCTACACAATATGGTCCAGAGTGCAGACGGCACG-
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replace(1115, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of decoxycholic acid or amide, cholic acid ande octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a to "to the propositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation to proportion of albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagonsis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease acting on glycoamino acide. This sequence represents DNA encoding a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
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11 Similarity 55.1%; Pred. No. 8.4e-100;
719; Conservative 0; Mismatches 570;
                                                                                                                                                                                                                                                                                     Sumitani J,
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                                                                                                                                                                                                                                                                                     Arai M,
                                          31-JAN-2001; 2001JP-00022953.
16-FEB-2001; 2001JP-00039796.
08-AUG-2001; 2001JP-00240002.
                                                                                                                                                                                                     (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                     Kouzuma T, Yoshioka I,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-599854/64.
P-PSDB; ABG30783.
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CACCGATATCAGCCGGGCATGATGTAAACAAACTTGCTGGCCGACTGTCGACTGCCGATA 190
                                                                                                                                                                                                                                               GCTCGCAGGAGGCCTGGATCGCCTGGGCGTCCGGGTACGTCCGGGCGAGGATCCTAATC 394
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                                                                                                                                                GGAAGAACGACCCGCTTTTCAAACCGTATTATCATGATACGGGCCTGCTGATGTCTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to compositions for assaying glycoprotein with use of protease and enzymes acting on glycoamino acids in the presence of at least 1 of deoxycholic acid or amide, cholic acid amide octyl glucoside, quaternary ammonium salt, quaternary ammonium salt cationic surfactant, concanavalin A and betaine and/or ascorbic oxidase and a buffer without a 4 (2-hydroxyethyl) 1-piperazinyl group. The invention also relates to compositions for assaying albumin containing the protease and enzymes for determining glycoalbumin and a protein-denaturing agent and/or a compound having S-S bond and bromocresol purple for evaluation of glycation having S-S bond and bromocresol purple for evaluation of glycation cate albumin into glycoalbumin with respect to the other albumins measured separately. The compositions are useful in clinical examination including diagnosis and management of diabetes. The compositions can be used in methods which avoid the effects of globulin and ascorbic acid components and stabilise enzymes such as protease acting on glycoamino acids. This sequence represents DNA encoding a polypeptide used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions for assaying glycoprotein without interference from globulin and ascorbic acid in blood, useful in clinical examination including diagnosis and management of diabetes.
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Local Similarity 55.1%; Pred. No. 8.4e-100;
Nes 719; Conservative 0; Mismatches 570; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel fructosylamine oxidase isolated from Pusarium proliferatum. The enzyme has the following physiochemical characteristics: (a) activity against fructosyllysine equivalent to or higher than that against fructosylvaline; (b) optimum pH for enzyme activity of 7.5; (c) enzyme stability optimally at 30-40 deg C; and (d) a molecular weight of about 39 kba as measured by SDS-PAGE and about 39.4 kba by gel filtration. Also disclosed is a similar Fructosylamine oxidase characterized by: (i) activity against fructosylvaline and no detectable activity against fructosylvaline and no detectable activity against fructosylvaline and no detectable activity against fructosylvaline and is modecular weight of about 49 kba as measured by SDS-PAGE and about 58 kba by gel filtration. The oxidases are useful in the measurement of Amadori compounds and particularly applicable in medical examination including for treatment and prevention of Galabetes by controlling serum glucose level for treatment and prevention of complications, and in food inspection. This sequence represents the coding sequence for the fructosylamine
                                                                                                                                                                                                                                                                                                                                                                                                           gene; fructosylamine oxidase; fructosyllysine; fructosylvaline;
lori compound; medical examination; diagnosis; serum glucose level;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusarium proliferatum-originated fructosylamine oxidase useful in measurement of Amadori compound and particularly applicable in medical examination including diagnosis and management of diabetes.
                                                                                                                                                                                                                                                                                                                                                         Fusarium proliferatum fructosylamine oxidase Q2 coding sequence
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                                                                    ATTTGCCCAAGAGTGTAGAGGGATGGACAATATCAAGAAT 1314
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/product= "fructosylamine oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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  CCAGAGAAAGTTTACGGAGTTCTGGGGTAAAGATCCCCTGGATCGGTTTGGAGCTGACGAT 1272
                                                                  ATTGTTGACGCGATGGAAGGTAAAGTGCCGCAAAAAATTCACGAATTAATCAAGTGGAAC 1221
                                                                                                          ATCTCTGATTGTATGGAGGGCACATTGGAGAAAGGTTTGCTAAGTTCTGGAGATGGCGA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to fructosylamine oxidase protein (I; ADS15771) and its coding sequence (II; ADS15772) from Pichia sp. preferably Pichia sp. NI-1 strain. (I) is useful for spectrosocpic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine compounds. (I) is also useful for analyzing fructosyl valine by spectroscopy, which involves degrading HbAlc, fructosamine or glycoalbumin in a sample using (I) to produce fructosylamine, respectively. (I) is also useful for carrying out electrochemical analysis of HbAlc, fructosamine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel fructosylamine oxidase protein, useful for spectroscopic analysis of fructosylamine compounds, and electrochemical analysis of fructosylamine and fructosyl valine compounds.
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                                                                                                                                                    CCGGACATTGCGGCGAACCGTAACTGGCGTGATACTCTGGGGGCGTTTTGGCGGGTCCAAAT
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236B production in ML-236B producing microbe.
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790 AATATACCGGTTATCTTTAACATCGAACGGGGGTTTTTCTTTGAACCCGATGAGGAGCGC
                                              739 recáricocarrargaaraarcrecaceraceracerreceaceracadaadarece
                                                                                                           850 GGTGAGATTAAAATATGCGATGAACACCCGGGCTACACAAATATGGTCCAGAGTGCAGAC
                                                                                                                                                                                                                      910 GCCACGATGATGAGCATTCCGTTCGAAAAAACCCAGA-----TTCCAAAAGAAGCC
                                                                                                                                                                                                                                                                          859 Accacreteccacacacacacacariterreascacceaccarescereceres
                                                                                                                                                                                                                                                                                                                                 961 GAAACGCGCGTTCGGGCCCTGCTGAAAGAGACAATGCCCCAGCTGGCAGACCGTCCATTC
                                                                                                                                                                                                                                                                                                                                                                                     919 GAAGCCCAAATGCGCCGGAACTTGCGACGTGTCCCCCCGAACTTGCAGACAAGACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a DNA sequence (I, ADE81173), which is associated with ML-255B synthesis. (I) is useful for improving ML-236B production in a HMG-COA reducing-enzyme-inhibitor ML-236B producing microbe. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                  ML-236B; HMG-CoA reducing enzyme; ds; Orf20
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TITAAATAICIGCCTICTAIIGGGAA 1157
                                           1066 TTCAAGATCATGCCAATCATTGGCAA 1091
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GCCGGGTGGCCAGCTGGTACAGCTATCGAGCGGATGGCAGGCGCTTCTCAGGAGAAA 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCTGCTCACAAAAGTCTCTTCCTGGCAACCGGCGGATCAGCACATGGGTTCAAGTTC 1300
                                                                                                                                                       CCAACCGCTTGGACCCTGGTACACATTGCGTTAAAACCGGAAGAACGTGCGTTGTACAAA 789
                                                                                                                                                                                                  790 AATATACCGGTTATCTTTAACATCGAACGGGGGTTTTTCTTTGAACCCGATGAGGAGCGC 849
                                                                                                                                                                                                                                              850 GGTGAGATTAAAATATGCGATGAACACCCGGGCTACACAAATATGGTCCAGAGTGCAGAC 909
                                                                                                                                                                                                                                                                                         GGCACGATGATGAGCATTCCGTTCGAAAAACCCAGA-----TTCCAAAAGAAGCC 960
                                                                                                           ACATTCCTGTGTGCTGGGGCTAGCGCGGGTCAGTTCCTAGATTTCAAGAATCAACTTCGA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCCTTCTATTGGGAATCTCATTGTTGACGCGATGGAAGGTAAAGTGCCGCAAAAAT 1199
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                                                                  A----ACGATGTAAAAGGTGCCGTTACGGGCGATGGCAAAATTTGGAGAGCGGAACGT
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                      GGTGTAAAATTTGTTACTGGCACCCCGCAGGGTCGTGTAGTCACGTTAATCTTTGAAAAT
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/product= "Fructosyl peptide oxidase"

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The present sequence is the coding sequence of Eupenicillium terrenum ATC 18547 cDNA encoding a novel fructosyl peptide oxidase (FPO). The CDNA was obtained by FOR and RACE amplification using primers based on peptide fragments of the purified enzyme. It is deposited in plasmid purces that the presence of oxygen and catalyse a reaction that produces alpha-ketoaldehyde, valyl histidine and hydrogen peroxide. The E. terrenum FPO exhibits 182% relative activity for fructosyl glycine and 9.78% for epsilon fructosyl lysine when compared to 100% activity for curchapy valyl histidine. It shows optimal activity in the phrange 6.0- The Km value for fructosyl valyl histidine. It shows optimal activity in the phrange 6.0- 3.00 and at temperatures up to about 45 degrees c. The Km value for fructosyl valyl histidine is 4.25 mm. The E. terrenum CDNA can be used for mass production of the enzyme by recombinant methods. Stable FPO enzymes usuch as E. terrenum FPO are useful in clinical diagnosis, e.g. of diabetes
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                                              1127 GACATTCCTTCAAGCTGTTGCCAAACATCGGGAAACACGTTGTTGAGGCTTTTAGAGGGAT 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fructosyl peptide oxidases useful as enzymes for clinical diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                      Kajiyama N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 34-36; 59pp; English
12-DEC-2001; 2001JP-00378151
06-AUG-2002; 2002JP-00228727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 48.2
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Kurosawa K, Hirokawa
                                                                                                                                                                                                                     (KIKK ) KIKKOMAN CORP
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P-PSDB; ABR41990.
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This sequence represents the coding sequence for the fructosyl amino acid oxidase (RAOD-P) of the invention. This sequence was isolated from Penicillium janthinellum 8-3413 (FERM BP-5475). FAOD-P oxidises amadori compounds in the presence of oxygen, producing alpha-kercaldehyde, amine derivatives and hydrogen peroxide. FAOD-P is used in the detection of smadori compounds in, e.g. foods such as soy sauce, and in body fluids such as blood. This sequence, vectors containing it and host cells transformed by the vector are all used for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fructosyl amino acid oxidase which oxidises amadori compounds and related DNA - used for detection of amadori compounds in foods and in body fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724 GCTCATATCCAACTCACGCCCAAGAATCGGCCCAGTACAAGGACGTGCCCGTAGTATAC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 GCTIGGAGTICGACGITAGIAGATITIGGAGGACCAAIGIGITITICGAAGGCCIGGGICTIC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTACACATTGCGTTAAAACCGGAAGAACGTGCGTTGTACAAAATATACCGGTTATCTTT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GGTGTTGAGACAGTAGATGGAACAAATACTTCGCCGACAAGGTGGTTTTGGCCGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               688 GCTAGCGCGCGTCAGTTCCTAGATTTCAAGAATCAACTTCGACCAACCGCTTGGACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 GGTGCCGTTACGGGCGATGCCAAAATTTGGAGAGCGGAACGTACATTCCTGTGTGCTGGG
                                                                                                                                                                                                                                                           Fructosyl amino acid oxidase; FAOD-P; enzyme; amadori compound; alpha-ketoaldehyde amine derivative; amadori detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%; Score 53.6; DB 2; Length 1314; 33.1%; Pred. No. 2.5e-06; ve 0; Mismatches 119; Indels 3.
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                                                                                                                                                                                                                          Coding sequence for fructosyl amino acid oxidase.
                                                                                                                    AAT85703 standard; cDNA to mRNA; 1314 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KYOT-) KYOTO DAIICHI KAGAKU CO LTD.
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1314
/*tag= a
868 GATGAACACCCGGGCT 883
                              841 GATGAATTTCCAGGTT 856
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Conservative
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                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                               Penicillium janthinellum.
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Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                 WO9721818-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1997.
                                                                                                                                                                                          16-FEB-1998
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                                                                                                                                                        AAT85703;
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1184 AAGTGCCGCAAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACCGTA 1243
                                1187 crcrarcecaecadarescrescrescresasaresasceses de reconstructor 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 GATGGTGATTATGGTTTTTTTTTTTGAACCAAAT---GAACATGGTGTTATAAAAGTTTGT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTGGTCTTCTACTTTAGTTGATTTTAGAAGATCAATGTGTTTTCTAAGGCTTGGGTTTTT 723
                                                                                                                                                                                                                                                                                                                               Fructosylamino acid oxidase; FAOD-P; Penicillium janthinellum S-3413; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present DNA sequence encodes a fructosylamino acid oxidase (FAOD-P). The present sequence is a synthetic sequence, derived from the wild type FAOD-P sequence of Penicillium janthinellum S-3413. The sequence was constructed using primers AAX15951-6006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA coding fructosylamino acid oxidase - synthetically designed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGTTGAAACTGTTGATGGTACTAAATATTTTGCTGATAAAGTTGTTTTAGCTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808 AACAICGAACGGGGTTTTTTTTTTTGAACCGGATGAGGAGCGCGGTGAGATTAAAATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628 GGTGCCGTTACGGGCGATGGCAAAATTTGGAGAGCGGAACGTACATTCCTGTGTGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCATATACAATTAACTCCACAAGAATCTGCTCAATATAAAGATGTTCCAGTTGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57.6; DB 2; Length 1314; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1314 BP; 408 A; 168 C; 244 G; 494 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                               a fructosylamino acid oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 8-10; 21pp; Japanese.
                                                                    1244 ACTGGCGTGATACTCTGG 1261
                                                                                                    1247 cracaccccrccrcccc 1264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOT-) KYOTO DAIICHI KAGAKU KK
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                                                                                                                                                                                          AAX15949 standard; DNA; 1314
                                                                                                                                                                                                                                                              (first entry)
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Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Penicillium janthinellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinantly prepared
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                                                                                                                                                                                                                                                                                               DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11046769-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1997;
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868 GATGAACACCCGGGCTACAC 887 |||||| || || || || 841 GATGAGTTCCCCGGGTTCTC 860

Search completed: May 29, 2005, 20:15:46 Job time : 844 Becs

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Tgestzyn9 StrPu691. Tgestzyf1 Tgestzyj9 Est07153

CK909112 CF684508 CF718110 CC797434 CC782545 AL437429 CC782545 AL302223 CC053986 CC3053986 CC3053986 CC3053986 CC3053986 CC3053989 AW309033 CC673989 AW309033 CC673989 AW309033 CC673989 AW309033 CC673989 AW309033 CC673989

T3 end of TgESTzyo7

CCABX24TR ZUAE111TV ZMMBBc045 Drosophil 4014786 1 2k10d07.r BX275202

TgESTzyce MCSA078E0

ZMMBBC049

TAM32-22K 8f94a10.y

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Sequence:

Minimum DB Maximum DB

Database

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Result

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Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
Tel: 504 286 4405
Fax: 504 286 4419
Email: jiuyu@srrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiuyu@srrc.ars.usda.gov) for clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CO142686
BST831357 Aspergillus flavus Normalized cDNA Expression Library
Aspergillus flavus cDNA clone NREESSO 5' end similar to (042629)
Fructosyl amine:oxygen oxidoreductase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotta; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
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/cell_type="mycelia"
/dev_Etage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10B T1 resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression
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/mol_type="mRNA"
/strain="NRRL 3357"
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                                                                     CC782545
CNS07BFZ
CO055263
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CD309225
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CO142686.1 GI:48896687
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Aspergillus flavus
information
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TITLE
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k2d07j2.r
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               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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CN2 41854
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CF8 71025
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CR901049
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9b_htc:*
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9b_est4:*
9b_est4:*
9b_est6:*
9b_gs81:*
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                                                                                                                                                                                                                                                                             Scoring table:
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/note="Vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site_1: Not1, at the 5

 $\mathtt{Library}^{\mathtt{n}}$

NCP2H3T7 mgxb0011E

AJ237240 tric088xc

AJ237240 / CF883318 (CB909424 t AA901536 AQ447867 AL435262

tric088xc

T3 end of CCABL49TF

CF684496

CF684496 AA901536 AQ447867

000

AJ237240 CF883318 CB909424

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prime end; Site_2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."
                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1048 GATACCGCGAATCGCGAATTCCTGATAGATCGACATCCGCAGTACCACACTCTTGTGTTG 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1108 GGCTGTGGTGCGAGCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAAATCTCATTGTT 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCGGGCTACACAATATGGTCCAGAGTGCAGA-----CGGCACGATGATGAGCATT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCCTGGATATTGCAACTTCGTCCCGGACCCGAAGCACGCGGTGAGGTGCGCAGTATC 493
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                                                                                                                                                                                                                                                                                                                                                        AAGAAGGCCATGTTCTCGGCATACACCGAAAGCAAAGCGCCTAGGAGTCACTTTCATCACC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 AGTGATCGTCTCTGGACTTTAAGAACAGCTCCGTCCTACCGCCTGGACGCTCTGCCAC 313
                                                                                                                                                                                                                                                                             GGCACCCCGCAGGGTCGTGTAGTCACGTTAATCTTTGAAAATAACGATGTAAAAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GGCTCCCCTGAAGGAGACGTTGTATCTCTAATTTACGAGAATGGAGACGTAGTCGGAGCC
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                                                                                                                                                           Length 782;
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                                                                                                                                                         16.7%; Score 237.4; DB 7; 58.8%; Pred. No. 8.8e-63;
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2 (bases 1 to 1040) Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.

11152876

MEDLINE PUBMED AUTHORS

REFERENCE

JOURNAL

20584711

Genomic exploration of the hemiascomycetous yeasts: 13. Pichia

FEBS Lett. 487 (1), 76-81 (2000)

(bases 1 to 1040)

REFERENCE AUTHORS

11152888

PUBMED

20584723

angusta

JOURNAL

TITLE

Eukaryotta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Pichia.

Saccharomycetales; Saccharomycetaceae; Pichia.

I (bases I to 1040)

Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Belotin-Fukuhara, M., Bon, E., Brottier, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekana, P., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Wincker, P. and Weissenbach, J.
Seconatic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

Pichia angusta

ORGANISM

SOURCE

AUTHORS

REFERENCE

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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefedgenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces textonia, and saccharomyces handenia, and saccharomyces handenia var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this insert.
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/note="similar to 043029 [Fructosyl amine; SPBC354.15 ] [
/note="similar to nombe ]"
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8.3%; Score 118.4; DB 9;
Best Local Similarity 50.5%; Pred. No. 3.1e-25;
Matches 380; Conservative 0; Mismatches 351;
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/mol_type="genomic DNA"
/strain="CBS 4732"
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/clone="XBB0AA002F11"
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CNS07A13 1040 bp DNA linear GSS 08-JUL-2001 T7 end of clone XBB0AA002F11 of library XBB0AA from strain CBS 4732 of Pichia angusta, genomic survey sequence.

DEFINITION

AL435997 AL435997.1 GI:12219410 GSS.

ACCESSION VERSION KEYWORDS

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T3 end of clone BC0AA003H11 of library BC0AA from strain CBS 767 of
Debaryomyces hansenii, genomic survey sequence.
                                                                                                                                                                             CAGATTCCAAAAGAAGCCGAAACGCGCGTTCGGGCCCTGCTGAAAGAGACAATGCCCCAG 1002
                                                                                                                                                                                                                                                     CTGGCAGACCGTCCATTCAGCTTCGCACGCATTTGCTGGTGTGCCGGATACCGCGAATCGC 1062
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                                                                                                       TACACAAATATGGTCCAGAGTGCAGACGGCACGATGATGAGGCATTCCGTTCGAAAAAACC 942
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ACCTCAGAAGAGGCTAAAAGCGCTGAAAAACTCTCCTGTTCTTTTGAACCTAGATGAAGGG 733
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lobases 1 to 906)

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Pukuhara, M., Bon, E., Brottier, P., Casaregola, S., Ge-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Teklaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Wincker, P. and Weissenbach, J.

Genomic exploration of the hemisascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                    rrccrrrrrgagccccaaaa---regearccraaagrrrrgcaaccagrrrccaga
                                   TTTTTCTTTGAACCCGATGAGGGCGCGGTGAGATTAAAATATGCGATGAACACCCGGGC
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Artiguenave, F., Wincker, P. and Gaillardin, C.
Genomic exploration of the hemiascomycetous yeasts: 14.
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to 043029 [ PUTATIVE FRUCTOSYL AMINO ACID OXIDASE ]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Debaryomyces hansenii"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99.2; DB 9;
Pred. No. 3.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 99.2;
50.8%; Pred. No. 3.3
Submitted (08-SEP-2000) Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="CBS 767"
/variety="hansenii"
/db xref="taxon:4959"
/clone="BC0AA003H1"
/clone lib="BC0AA003H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . >716
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Best Local Similarity
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457 423

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/db_xref="taxon:5514"
/clone=lay4902fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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338 CGCAGGAGGCCCTGGATCGCCTGGGCGTCCGGGTACGTCCGGGCGAGGATCCTAATCTGG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
234 3e-19 gi|2661130|gb|AABB82 (AF035700) fructosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium sporotrichioides
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 AGGACGATGCAATGCCTCATGTTGACAAGTACATTAGCACCTGCAGAGA---TAAACTCC
                                                                                                                                     398 TGGAACTTACCCGCCCGGAGCAATTTCGTAAACTGGCCCCCGGGAAGGCGTGTTGCAAGGTG
                                                                                                                                                                                                      364 GGTTACTCAACTCGGCCGCGGATTTCAGAGCTACAATGCCGTTGGGCGTCCTGACAGGGG
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Contact: Bruce A. Ree, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Partington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B. Analysis of a Fusarium sporotrichioides EST database Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 253.
Location/Qualifiers
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/strain="Tri 10"
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Best Local Similarity 53.3
Matches 153; Conservative
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BI187569/c
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KEYWORDS
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AUTHORS
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/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
                            AA787493 440 bp mRNA linear EST 31-JUL-1998 n5a03a1.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

I (bases 1 to 440)

Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

An Aspergillus nidulans EST Database
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912

Fax: 405 325 7762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emericella nidulans (anamorph: Aspergillus nidulans)
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/organism="Emericella nidulans"
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We anticipate the future release of
Genetics Stock Center
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/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="n5a03a1"
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AA787493
AA787493.1 GI:2847724
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
E 1 (bases 1 to 414)
Is Ren, Q., Tad, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,
Beremand, M. and Roe, B.
Analysis of a Rusarium sporotrichioides EST database
Unpublished (2001)
Other ESTs: a4902fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
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/clone="a4g02fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
TCAACGGCTCTGCACCTCGCGCGCGCGCGGATATACCAACGTTACCGTGCTGGACCCCTAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 accarcccrrcaccarcrcrecesescarcarerereacaacarrecaastrecaastreaar 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 217 3e-29 gi|2661130|gb|AAB882 (AF035700) fructosyl amine:oxygenoxidoredu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
                                                                                                                                                                                                                                     BI187570 414 bp mRNA linear EST 10-JUL-a4g02fs.rl Fusarium sporotrichioides Tri 10 overexpressed CDNA library Fusarium sporotrichioides CDNA clone a4g02fs 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GCTCTCGCCGTCACTAAGTCATCATCTCTCCTGATCGTTGGTGCCGGGACTTGGGGCCACC
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Location/Qualifiers
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Fusarium sporotrichioides
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/strain="Tri 10"
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Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paracoccidioides brasiliensis

Paracoccidioides brasiliensis

Bukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Buygenales; mitosporic Onygenales; Paracoccidioides.

I (bases 1 to 677)

Simose, I.C., Andrade, R.V., Araes, F.B.M.,

Simose, I.C., Andrade, E.V., Maranhao, A.Q., Torres, F.A.G.:

Jesuino, R.S.A., Kyaw, C.M., Marashao, A.Q., Torres, F.A.G.:

Jesuino, R.S.A., Kyaw, C.M., Marashao, M.P., Nicola, A., Pereira, M.,

Walter, M.E.M.T., Soares, C.M.A. and Brigido, M.M.

Metabolic features of Paracoccidioides brasiliensis cell

differentiation as accessed by transcriptome analysis

LOndract: Pelippe MSS

Laboratory of Molecular Biology

Institute of Biology - University of Brasilia

Campus Universitatio, Asa Norte, Brasilia, DF 70910-900, BRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Mycelium and yeast cells from Paracoccidioides brasilTensis"
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                                                                     1191 GCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACCGTAACTGGCG 1250
                                                                                                                                                                                                                                                                                                                                     EST 09-APR-2004
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277 ATACAAGCACATTACATCTATTGGCAAATTCATCTGGATTGTATGGAGGGTAGATTGGA 218
                                                                                                                   217 AGAGAGATTTGCCAAGTTTTGGACATGGAGACCCGGAGAGTTTACTGAGTTTTGGGGTAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAAAAAAACCCAGATTCCAAAAGAAGCCGAAACGCGCGTTCGGGCCCTGCTGAAAGAGAC 992
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                                                                                                                                                                  1251 TGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGATGGATTTTC 1297
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                                                                                                                                                                                                CGATCCTCTAGATCGATTTGGTGCTGACGATACTATCATGGATCTGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism≈"Paracoccidioides brasiliensis"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Pb01"
                                                                                                                                                                                                                                                                                                                                                                                                                              CN241854.1 GI:46345598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 55 61 307 2423
Fax: 55 61 349 8411
Email: msueli@unb.br
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/ Geell type="mycelium"

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/cloe lib="Magnaporthe grisea NS Uni-Zap XR Library"

/cloe lib="Magnaporthe grisea NS Uni-Zap XR Library"

/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:

XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.

Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium baseled with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence was trimed according to the alignment, otherwise sequence guality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                        mgns007xF15f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns007xF15 5', mRNA sequence.
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Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person, Best nr hit (April. 22, 2003) gb|EAA30984.1| hypothetical
protein [Neurospora crassa] 194 6e-49
PCR PRimers
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Expressed sequence tags from the rice blast fungus, Magnaporthe
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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Magnaporthe grisea
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/mol_type="mRNA"
/strain="Guyll"
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clone="mgns007xF15"
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/note="Vector: pSPORT1; Library constructed from cultures
grown in Czapek Dox for 3 days then Glucose Yeast Nitrogen
Base for 1 day, shift of nitrogen source from nitrate to
ammonium ions"
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AJ616269 MgA Mycosphaerella graminicola cDNA clone mga1757f, mRNA
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Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A.

A group of expressed crolNA sequences from the wheat fungal leaf

Bolotch pathogen, Wycosphaerella graminicola (Septoria tritici)

Fungal Genet. Biol. 29 (2), 118-133 (2000)
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/mol_type="mRNA"
/strain="Strit"
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Insert Length: 800 Std Error: 100.00
Seg primer: M13 reverse.
Location/Qualifiers
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Plant Pathogen Interactions Division,
Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44(0)1582 763133
Fax: +44(0)1582 76981
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/clone="mga1757f"
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Crytococcus neoformans var. neoformans
Bukaryota, Pungi, Basidicmycota, Hymenomycetes,
Heterobasidiomycetes, Tremellomycetidae, Tremellales, Tremellaceae,
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                                                                               GTGGTGCGAGCGGAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGACG 1171
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CCGCGAATCGCGAATTCCTGATAGATCGACATCCGCAGTACCACAGTCTTGTGTTGGGCT 1111
                          CAAAGTCGGGCGATTTCATCGATTACCATCCTGAGTGGGAAGGTCTTTTCCTCGCCA 336
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Tel: 405-271-2133 ex2133
Email: juneann-murphy@ouhsc.edu
This clone is available from the Fungal Genetics Stock Center,
This clone is available from the Pungal Genetics Stock Center,
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This clone is available from the Fungal Genetics Stock Center,
This clone is available from the Fungal Genetics Stock
This contact
This clone is available from the Fungal General For Interval Dr. Juneann Murphy(juneann-murphy@ouhsc.edu) for library
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k2d07j2.fl Cryptococcus neoformans strain B3501 Cryptococcus
neoformans var. neoformans cDNA clone k2d07j2 3', mRNA sequence.
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Roe, B.A. and Murphy, J.W.
Comparison of highly conserved intronic and exonic elements associated with splicing among five diverse fungal organisms Unpublished (2003)
Other ESTS: k2607j2.rl
Contact: Murphy, JW
Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
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/clone="k2d07j2"
/lab host="E. coli strain SOLR"
/clone_lib="Cryptococcus neoformans strain B3501"
/note="Vector: pBluescript sk-; Site 1: EcoRI at 5'
cDNA insert; Site_2: XhoI at 3' end of cDNA insert"
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/mol_type="mRNA"
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Pred. No. 5.2e-08;
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1 (bases 1 to 422)
Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.

The Est database from Sorghum: developing embryos
Unpublished (2000)
Contact: Cordonnier-Pratt MM
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 5.3e-06;
0; Mismatches 205; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 AATGTCCGAGCAGAGAAGTATGCTTGGAGGTGGAGACCTG 161
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                                                                                                                                                                                                                                                             EST 02-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mkNa" | from 1 | from 1 | from 1 | from 1 | from 2 | from 2 | from 2 | from 2 | from 2 | from 2 | from 2 | from 2 | from 2 | from 2 | from 3 | from 2 | from 3 | from 3 | from 3 | from 2 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | from 3 | fr
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tric025xe08 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric025xe08, mRNA sequence.
                                                                                                                                                                                                                                                                                                 tric025x017 T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tric025x017, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypocrea Jecuji, Ascomycota; Pezizomycotina; Sordariomycetes; Bukaryota; Pungi; Ascomycota; Hypocreacea; Hypocreacea; Hypocreacea; Hypocrean, Coreacea; Hypocreacea;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 CATCICCIGAICGIIGGIGCCGGGACIIGGGGCACCICAACGGCICIGCACCICGCGC
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CB901049.1 GI:30115707
EST
Hypocrea jecorina (anamorph: Trichoderma reesei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925 Page Mill Road, Palo Alto, CA 94304, USA
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Best Local Similarity 60.8%; Pred. No. 2.4e-05;
Matches 90; Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hypocrea jecorina"
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466 CCTCCCACGACATCAACAAGATCGTTCG 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Pamela K. Foreman
                                                                                                                                                                                                                                                                                                                                                                                                                                         CB901239.1 GI:30115897
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CB901049
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    1124 GAAGAGGGTTTAAATATCTGCCTTCTATTGGGAATCTCATTGTTGACGCGATGGAAGGTA 1183
                                                                                                                                                                                1184 AAGTGCCGCAAAAATTCACGAATTAATCAAGTGGAACCCGGACATTGCGGCGAACCGTA 1243
                                                                                                                                                                                                                                                                                                                                                       1244 ACTGGCGTGATACTCTGGGGCGTTTTTGGCGGTCCAAATCGTGTGATGGATTTTCATGATG 1303
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Hypocrea jecorina
Bukaryota; Fundi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

(bases 1 to 758)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 CATCTCCTGATCGTTGGTGCCGGGACTTGGGGCACCTCAACGGCTCTGCACCTCGCGC 112
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                                                                                                                                                                                                                                                             260 AACCACGGGATGACTTGGGTACTGAATTCCAGAAGAGTGGTCATGGCCGAAGCAGAAGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                         320 Accaerrrigarcacareregacgaacgaeregagagagagagagagagagagarigarigarig
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/clone="tricolor"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
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Contact: Ralph A. Dean
Fungal Genomics Laboratory
Courth Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
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/mol_type="mRNA"
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Seg primer: LT-F1 primer.
Location/Qualifiers
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Fax: 919-513-0024
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CFB70843 B22 bp mRNA linear EST 31-OCT-2003 tric025xe08.bl T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric025xe08, mRNA sequence. CFB70843
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/clone="tric025xe08"

/dev stage="mycelia"

/clone_lib="T.reesei mycelial culture, Version 3 april"

/note="Vector: pREP3Y; Site_1: Not I/Sal 1; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

and Nitrogen sources and concentrations."
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1. (bases 1 to 822)

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1. contaissen, P., Houfek, T.D.,

Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,

Ward, M. and Dean, R.A.
                                      Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 822)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dun-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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925 Page Mill Road, Palo Alto, CA 94304, USA
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Fax: (650) 621-7817
Email: Pforeman@genencor.com
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Location/Qualifiers
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Fungal Genomics Laboratory
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/clone="tric025xe08"
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2003"
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Campus Box 7251, Raleigh, NC 27695, USA Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: IT-F1 primer.
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/organism="Hypocrea jecorina"
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